

## SEQUENCE LISTING

<110> Heard, Jacqueline  
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 Zhang, James  
 Benito, Maria-Ines  
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 Fromm, Mike

<120> PLANT GENE SEQUENCES I

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Lys Arg Ser Asp Phe Phe Asp Leu Asp Asp Asp Phe Glu Ala Asp Phe	
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Ala Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile	
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cac His	tgg Trp	ttg Leu	aat Asn	ctt Leu	tct Ser	tct Ser	tta Leu	caa Gln	aga Arg	aat Asn	aca Thr	cag Gln	aaa Lys	atg Met	gtg Val	457
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270275280285																



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Leu	Tyr	Gly	Lys	Gln	Ser	Ser	Ile	Phe	Leu	Pro	Met	Ala	Thr	Met	Lys	
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Pro	Leu	Lys	Thr	Val	Ala	Ala	Ser	Ser	Gly	Phe	Pro	Phe	Ile	Ser	Met	
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aca	agt	tcc	tct	tcc	tcc	atg	tcc	aat	tgt	ttt	gat	cca	tagg	atcgtt		1178
Thr	Ser	Ser	Ser	Ser	Ser	Met	Ser	Asn	Cys	Phe	Asp	Pro				
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Asn	Ser	Ser	Ser	Ser	Ser	Thr	Thr	Asp	Ser	Ala	Ala	Arg	Asp	Ala	Phe	
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Ile	Ala	Phe	Gly	Ile	Leu	Lys	Arg	Asp	Asp	Asp	Leu	Val	Pro	Pro	Pro	
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Pro	Pro	Pro	Pro	His	Lys	Glu	Thr	Gly	Asp	Leu	Phe	Pro	Val	Val	Ala	
65					70				75						80	
Asp	Ala	Arg	Arg	Asn	Ile	Glu	Phe	Ser	Val	Glu	Asp	Ser	His	Trp	Leu	
				85					90					95		
Asn	Leu	Ser	Ser	Leu	Gln	Arg	Asn	Thr	Gln	Lys	Met	Val	Lys	Lys	Ser	
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Arg	Arg	Gly	Pro	Arg	Ser	Arg	Ser	Ser	Gln	Tyr	Arg	Gly	Val	Thr	Phe	
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Tyr	Arg	Arg	Thr	Gly	Arg	Trp	Glu	Ser	His	Ile	Trp	Asp	Cys	Gly	Lys	
	130					135					140					

Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala Tyr Ala Ala Ala Arg Ala  
 145 150 155 160  
 Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Leu Asp Ala Asp Ile Asn  
 165 170 175  
 Phe Val Val Asp Asp Tyr Arg His Asp Ile Asp Lys Met Lys Asn Leu  
 180 185 190  
 Asn Lys Val Glu Phe Val Gln Thr Leu Arg Arg Glu Ser Ala Ser Phe  
 195 200 205  
 Gly Arg Gly Ser Ser Lys Tyr Lys Gly Leu Ala Leu Gln Lys Cys Thr  
 210 215 220  
 Gln Phe Lys Thr His Asp Gln Ile His Leu Phe Gln Asn Arg Gly Trp  
 225 230 235 240  
 Asp Ala Ala Ala Ile Lys Tyr Asn Glu Leu Gly Lys Gly Glu Gly Ala  
 245 250 255  
 Met Lys Phe Gly Ala His Ile Lys Gly Asn Gly His Asn Asp Leu Glu  
 260 265 270  
 Leu Ser Leu Gly Ile Ser Ser Ser Ser Glu Ser Ile Lys Leu Thr Thr  
 275 280 285  
 Gly Asp Tyr Tyr Lys Gly Ile Asn Arg Ser Thr Met Gly Leu Tyr Gly  
 290 295 300  
 Lys Gln Ser Ser Ile Phe Leu Pro Met Ala Thr Met Lys Pro Leu Lys  
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 Ser Ser Ser Met Ser Asn Cys Phe Asp Pro  
 340 345

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 <212> DNA  
 <213> Arabidopsis thaliana

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 <222> (377)..(1159)  
 <223> G974

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 cgtatagaag aaaactgatt tcttggtttg tattttctta aagagatcaa tcttttttta 180

tttttgatct	tcttggtgtt	ttttttcttt	gtagaattaa	tcgtttgtga	gggtattttt	240										
ttaattccct	cctctcagaa	atctacacag	aggtttttta	ttttataaac	ctcttttttcg	300										
attttcttga	aaacaaaaaa	tcctgttctt	tacttttttt	acaagaacaa	gggaaaaaaa	360										
tttcttttta	ttagaa	atg	aca	act	tct	atg	gat	ttt	tac	agt	aac	aaa	acg	412		
		Met	Thr	Thr	Ser	Met	Asp	Phe	Tyr	Ser	Asn	Lys	Thr			
		1				5					10					
ttt	caa	caa	tct	gat	cca	ttc	ggg	ggg	gaa	tta	atg	gaa	gcg	ctt	tta	460
Phe	Gln	Gln	Ser	Asp	Pro	Phe	Gly	Gly	Glu	Leu	Met	Glu	Ala	Leu	Leu	
		15					20				25					
cct	ttt	atc	aaa	agc	cct	tcc	aac	gat	tca	tcc	gcg	ttt	gcg	ttc	tct	508
Pro	Phe	Ile	Lys	Ser	Pro	Ser	Asn	Asp	Ser	Ser	Ala	Phe	Ala	Phe	Ser	
		30				35					40					
cta	ccc	gct	cca	att	tca	tac	ggg	tcg	gat	ctc	cac	tca	ttt	tct	cac	556
Leu	Pro	Ala	Pro	Ile	Ser	Tyr	Gly	Ser	Asp	Leu	His	Ser	Phe	Ser	His	
	45				50					55					60	
cat	ctt	agt	cct	aaa	ccg	gtc	tca	atg	aaa	caa	acc	ggg	act	tcc	gcg	604
His	Leu	Ser	Pro	Lys	Pro	Val	Ser	Met	Lys	Gln	Thr	Gly	Thr	Ser	Ala	
				65				70						75		
gct	aaa	ccg	acg	aag	cta	tac	aga	gga	gtg	aga	caa	cgt	cac	tgg	gga	652
Ala	Lys	Pro	Thr	Lys	Leu	Tyr	Arg	Gly	Val	Arg	Gln	Arg	His	Trp	Gly	
			80					85					90			
aaa	tgg	gtg	gct	gag	att	cgt	tta	ccg	agg	aat	cga	act	cga	ctt	tgg	700
Lys	Trp	Val	Ala	Glu	Ile	Arg	Leu	Pro	Arg	Asn	Arg	Thr	Arg	Leu	Trp	
		95				100						105				
ctc	gga	aca	ttc	gac	acg	gcg	gag	gaa	gct	gct	tta	gct	tat	gac	aag	748
Leu	Gly	Thr	Phe	Asp	Thr	Ala	Glu	Glu	Ala	Ala	Leu	Ala	Tyr	Asp	Lys	
	110					115					120					
gcg	gcg	tat	aag	ctc	cga	gga	gat	ttt	gcg	cgg	ctt	aat	ttc	cct	gat	796
Ala	Ala	Tyr	Lys	Leu	Arg	Gly	Asp	Phe	Ala	Arg	Leu	Asn	Phe	Pro	Asp	
	125				130					135					140	
ctc	cgt	cat	aac	gac	gag	tat	caa	cct	ctt	caa	tca	tca	gtc	gac	gct	844
Leu	Arg	His	Asn	Asp	Glu	Tyr	Gln	Pro	Leu	Gln	Ser	Ser	Val	Asp	Ala	
			145					150						155		
aag	ctt	gaa	gct	att	tgt	caa	aac	tta	gct	gag	acg	acg	cag	aaa	cag	892
Lys	Leu	Glu	Ala	Ile	Cys	Gln	Asn	Leu	Ala	Glu	Thr	Thr	Gln	Lys	Gln	
			160				165						170			
gtg	aga	tca	acg	aag	aag	tct	tct	tct	cgg	aaa	cgt	tca	tca	acc	gtc	940
Val	Arg	Ser	Thr	Lys	Lys	Ser	Ser	Ser	Arg	Lys	Arg	Ser	Ser	Thr	Val	
		175				180						185				
gca	gtg	aaa	cta	ccg	gag	gag	gac	tac	tct	agc	gcc	gga	tct	tcg	ccg	988
Ala	Val	Lys	Leu	Pro	Glu	Glu	Asp	Tyr	Ser	Ser	Ala	Gly	Ser	Ser	Pro	
	190															

Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe  
100 105 110

Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr Lys  
 115 120 125  
 Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asp Leu Arg His Asn  
 130 135 140  
 Asp Glu Tyr Gln Pro Leu Gln Ser Ser Val Asp Ala Lys Leu Glu Ala  
 145 150 155 160  
 Ile Cys Gln Asn Leu Ala Glu Thr Thr Gln Lys Gln Val Arg Ser Thr  
 165 170 175  
 Lys Lys Ser Ser Ser Arg Lys Arg Ser Ser Thr Val Ala Val Lys Leu  
 180 185 190  
 Pro Glu Glu Asp Tyr Ser Ser Ala Gly Ser Ser Pro Leu Leu Thr Glu  
 195 200 205  
 Ser Tyr Gly Ser Gly Gly Ser Ser Ser Pro Leu Ser Glu Leu Thr Phe  
 210 215 220  
 Gly Asp Thr Glu Glu Glu Ile Gln Pro Pro Trp Asn Glu Asn Ala Leu  
 225 230 235 240  
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 Ser Ser Leu Val Asn  
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 <213> Arabidopsis thaliana

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 <222> (58)..(654)  
 <223> G975

<220>  
 <223> "n" at various positions throughout the sequence  
 may be A, T, C, G, other or unknown

<220>  
 <223> Xaa at amino acid position 90 is either a Serine  
 or not present

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 atg gta cag acg aag aag ttc aga ggt gtc agg caa cgc cat tgg ggt 105  
 Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly  
 1 5 10 15

tct tgg gtc gct gag att cgt cat cct ctc ttg aaa cgg agg att tgg 153  
Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp  
20 25 30

cta ggg acg ttc gag acc gca gag gag gca gca aga gca tac gac gag 201  
Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu  
35 40 45

gcc gcc gtt tta atg agc ggc cgc aac gcc aaa acc aac ttt ccc ctc 249  
Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu  
50 55 60

aac aac aac aac acc gga gaa act tcc gag ggc aaa acc gat att tca 297  
Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser  
65 70 75 80

gct tgc tcc aca atg tca tcc tca aca tma tct tca tgc ctc tct tcc 345  
Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser  
85 90 95

atc ctc agc gcc aaa ctg agg aaa tgc tgc aag tct cct tcc cca tcc 393  
Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser  
100 105 110

ctc acc tgc ctc cgt ctt gac aca gcc agc tcc cat atc ggc gtc tgg 441  
Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp  
115 120 125

cag aaa cgg gcc ggt tca aag tct gac tcc agc tgg gtc atg acg gtg 489  
Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val  
130 135 140

gag cta ggt ccc gca agc tcc tcc caa gag act act agt aaa gct tca 537  
Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser  
145 150 155 160

caa gac gct att ctt gct ccg acc act gaa gtt gaa att ggt ggc agc 585  
Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser  
165 170 175

aga gaa gaa gta ttg gat gag gaa gaa aag gtt gct ttg caa atg ata 633  
Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile  
180 185 190

gag gag ctt ctc aat aca aac taaatcttat ttgcttatat atatgtacct 684  
Glu Glu Leu Leu Asn Thr Asn  
195

atcttcattg ctgatttaca gccaaaataa tcaattatac cgtgtatttt atagatgttt 744

tatattaaaa ggttggttaga tatananana nnnnnnnnnn ananannnna a 795

<210> 28  
<211> 199  
<212> PRT  
<213> Arabidopsis thaliana

&lt;220&gt;

&lt;223&gt; G975

&lt;220&gt;

<223> Xaa at amino acid position 90 is either a Serine  
or not present

&lt;400&gt; 28

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20 25 30Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu  
35 40 45Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu  
50 55 60Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser  
65 70 75 80Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser  
85 90 95Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser  
100 105 110Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp  
115 120 125Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val  
130 135 140Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser  
145 150 155 160Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser  
165 170 175Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile  
180 185 190Glu Glu Leu Leu Asn Thr Asn  
195

&lt;210&gt; 29

&lt;211&gt; 966

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (72)..(815)

&lt;223&gt; G976

G975: 28-195

&lt;220&gt;

<223> "n" at various positions throughout the sequence  
may be A, T, C, G, other or unknown

&lt;220&gt;

<223> Xaa at amino acid position 77 may be various or  
unknown

&lt;400&gt; 29

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      Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala
        1              5              10

ata atc caa tct tct act tca tcg tca gtt act att gtg cca gtt ccc 158
Ile Ile Gln Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro
      15              20              25

acg tgc ggt gac agc ctc tct gac tct gcc acg tgt gaa aac cct tgt 206
Thr Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys
      30              35              40              45

cca ctt gat act atc act act act act act gtt tgt ttt gcg gct 254
Pro Leu Asp Thr Ile Thr Thr Thr Thr Thr Val Cys Phe Ala Ala
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cct tct tct act gca agt ggt aat gat att aat act tta atg gcc nct 302
Pro Ser Ser Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Xaa
      65              70              75

gac acc gac atc tct cgc cgg aaa aag aat ccg gtt tat cgg gga att 350
Asp Thr Asp Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile
      80              85              90

cgt tgt cgg agt gga aaa tgg gtg tct gaa atc cga gag cct aaa aag 398
Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys
      95              100              105

act aca cgt gtc tgg ctt ggg act tat ccg acg ccg gag atg gct gct 446
Thr Thr Arg Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala
     110              115              120              125

gcc gca tat gac gtg gcg gcg tta gct ctt aaa ggt gga gac act ctc 494
Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu
      130              135              140

ttg aac ttc ccg gat tcc ctg gga tct tac ccc att ccc ata tct tct 542
Leu Asn Phe Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser
      145              150              155

tcc gca gct cat atc aga tgc gct gca gct gcg gct gct gcg act agg 590
Ser Ala Ala His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg
      160              165              170

ggg gcg gct gga gcg gcc gtg aag gta ggt caa aag aag gaa gat aaa 638
Gly Ala Ala Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys
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CCLE 60-6151660



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Asp	Ser	Leu	Ser	Asp	Ser	Ala	Thr	Cys	Glu	Asn	Pro	Cys	Pro	Leu	Asp	
		35					40					45				
Thr	Ile	Thr	Thr	Thr	Thr	Thr	Thr	Val	Cys	Phe	Ala	Ala	Pro	Ser	Ser	
	50						55				60					
Thr	Ala	Ser	Gly	Asn	Asp	Ile	Asn	Thr	Leu	Met	Ala	Xaa	Asp	Thr	Asp	
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Ile	Ser	Arg	Arg	Lys	Lys	Asn	Pro	Val	Tyr	Arg	Gly	Ile	Arg	Cys	Arg	
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may be A, T, C, G, other or unknown
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Gln	Gln	Arg	Phe	Arg	Gly	Val	Arg	Gln	Arg	His	Trp	Gly	Ser	Trp	Val	
5					10					15					20	
tcc	gaa	att	cgt	cac	cct	ctc	ttg	aaa	aca	aga	atc	tgg	cta	ggg	acg	153
Ser	Glu	Ile	Arg	His	Pro	Leu	Leu	Lys	Thr	Arg	Ile	Trp	Leu	Gly	Thr	
				25					30					35		
ttt	gag	aca	gcg	gag	gat	gca	gca	agg	gcc	tac	gac	gag	gcg	gct	agg	201
Phe	Glu	Thr	Ala	Glu	Asp	Ala	Ala	Arg	Ala	Tyr	Asp	Glu	Ala	Ala	Arg	
			40					45					50			

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cta atg tgt ggc ccg aga gct cgt act aat ttc cca tac aac cct aat 249
Leu Met Cys Gly Pro Arg Ala Arg Thr Asn Phe Pro Tyr Asn Pro Asn
      55                      60                      65

gcc att cct act tcc tct tcc aag ctt cta tca gca act ctt acc gct 297
Ala Ile Pro Thr Ser Ser Ser Lys Leu Leu Ser Ala Thr Leu Thr Ala
      70                      75                      80

aaa ctc cac aaa tgc tac atg gct tct ctt caa atg acc aag caa acg 345
Lys Leu His Lys Cys Tyr Met Ala Ser Leu Gln Met Thr Lys Gln Thr
      85                      90                      95                      100

caa aca caa acg caa acg cag acc gca aga tca caa tcc gcg gac agt 393
Gln Thr Gln Thr Gln Thr Gln Thr Ala Arg Ser Gln Ser Ala Asp Ser
      105                      110                      115

gac ggt gtg acg gct aac gaa agt cat ttg aac aga gga gta acg gag 441
Asp Gly Val Thr Ala Asn Glu Ser His Leu Asn Arg Gly Val Thr Glu
      120                      125                      130

acg aca gag atc aag tgg gaa gat gga aat gcg aat atg caa cag aat 489
Thr Thr Glu Ile Lys Trp Glu Asp Gly Asn Ala Asn Met Gln Gln Asn
      135                      140                      145

ttt agg cca ttg gag gaa gat cat atc gag caa atg att gag gag ctg 537
Phe Arg Pro Leu Glu Glu Asp His Ile Glu Gln Met Ile Glu Glu Leu
      150                      155                      160

ctt cac tac ggt tcc att gag ctt tgc tct gtt tta cca act cag acg 585
Leu His Tyr Gly Ser Ile Glu Leu Cys Ser Val Leu Pro Thr Gln Thr
      165                      170                      175                      180

ctg tgagaaatgg ccttgctcgtt ttagcgtatt cttttcattt ttatttttgt 638
Leu

ttccacaaaa acggcgtcgt aagtgatgag agtagtagtg agagaaggct aatttcaaga 698

cattttgatc tgaattggcc tcttttgaaa cactgattct agtttctata agagcaatcg 758

atcatatgct atgttatgta tagtattata aaaaaatggt attttctgat tnaaaaaaaaa 818

aaaaaaaaaa aaaaaa 833

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<211> 181
<212> PRT
<213> Arabidopsis thaliana

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<220>
<223> G977

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<400> 32
Met Ala Arg Pro Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp
  1                      5                      10                      15

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<210> 33
<211> 1530
<212> DNA
<213> Arabidopsis thaliana
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<220>
<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown
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<400> 33
cctctgagga atcaaattcac tcacactcca aaaaaaaatc taaactttct cagagtttta 59
atg aag aag cgc tta acc act tcc act tgt tct tct tct cca tct tcc 107
Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
  1          5          10          15
tct gtt tct tct tct act act act tcc tct cct att cag tcg gag gct 155
Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
          20          25          30

```

cca	agg	cct	aaa	cga	gcc	aaa	agg	gct	aag	aaa	tct	tct	cct	tct	ggt	203
Pro	Arg	Pro	Lys	Arg	Ala	Lys	Arg	Ala	Lys	Lys	Ser	Ser	Pro	Ser	Gly	
		35					40					45				
gat	aaa	tct	cat	aac	ccg	aca	agc	cct	gct	tct	acc	cga	cgc	agc	tct	251
Asp	Lys	Ser	His	Asn	Pro	Thr	Ser	Pro	Ala	Ser	Thr	Arg	Arg	Ser	Ser	
	50					55					60					
atc	tac	aga	gga	gtc	act	aga	cat	aga	tgg	act	ggg	aga	ttc	gag	gct	299
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Phe	Glu	Ala	
	65				70					75					80	
cat	ctt	tgg	gac	aaa	agc	tct	tgg	aat	tcg	att	cag	aac	aag	aaa	ggc	347
His	Leu	Trp	Asp	Lys	Ser	Ser	Trp	Asn	Ser	Ile	Gln	Asn	Lys	Lys	Gly	
				85					90					95		
aaa	caa	gtt	tat	ctg	gga	gca	tat	gac	agt	gaa	gaa	gca	gca	gca	cat	395
Lys	Gln	Val	Tyr	Leu	Gly	Ala	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ala	His	
		100						105					110			
acg	tac	gat	ctg	gct	gct	ctc	aag	tac	tgg	gga	ccc	gac	acc	atc	ttg	443
Thr	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Asp	Thr	Ile	Leu	
		115					120					125				
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Asn	Phe	Pro	Ala	Glu	Thr	Tyr	Thr	Lys	Glu	Leu	Glu	Glu	Met	Gln	Arg	
	130					135					140					
gtg	aca	aag	gaa	gaa	tat	ttg	gct	tct	ctc	cgc	cgc	cag	agc	agt	ggt	539
Val	Thr	Lys	Glu	Glu	Tyr	Leu	Ala	Ser	Leu	Arg	Arg	Gln	Ser	Ser	Gly	
	145				150					155					160	
ttc	tcc	aga	ggc	gtc	tct	aaa	tat	cgc	ggc	gtc	gct	agg	cat	cac	cac	587
Phe	Ser	Arg	Gly	Val	Ser	Lys	Tyr	Arg	Gly	Val	Ala	Arg	His	His	His	
				165					170					175		
aac	gga	aga	tgg	gag	gct	cgg	atc	gga	aga	gtg	ttt	ggg	aac	aag	tac	635
Asn	Gly	Arg	Trp	Glu	Ala	Arg	Ile	Gly	Arg	Val	Phe	Gly	Asn	Lys	Tyr	
			180					185					190			
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Leu	Tyr	Leu	Gly	Thr	Tyr	Asn	Thr	Gln	Glu	Glu	Ala	Ala	Ala	Ala	Tyr	
		195					200					205				
gac	atg	gct	gcg	att	gag	tat	cga	ggc	gca	aac	gcg	gtt	act	aat	ttc	731
Asp	Met	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Ala	Asn	Ala	Val	Thr	Asn	Phe	
	210					215					220					
gac	att	agt	aat	tac	att	gac	cgg	tta	aag	aag	aaa	ggt	gtt	ttc	ccg	779
Asp	Ile	Ser	Asn	Tyr	Ile	Asp	Arg	Leu	Lys	Lys	Lys	Gly	Val	Phe	Pro	
	225				230					235					240	
ttc	cct	gtg	aac	caa	gct	aac	cat	caa	gag	ggg	att	ctt	gtt	gaa	gcc	827
Phe	Pro	Val	Asn	Gln	Ala	Asn	His	Gln	Glu	Gly	Ile	Leu	Val	Glu	Ala	
				245					250					255		

aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa 875  
 Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu  
 260 265 270

gtg aaa caa cag tac gtg gaa gaa cca ccg caa gaa gaa gaa gag aag 923  
 Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys  
 275 280 285

gaa gaa gag aaa gca gag caa caa gaa gca gag att gta gga tat tca 971  
 Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser  
 290 295 300

gaa gaa gca gca gtg gtc aat tgc tgc ata gac tct tca acc ata atg 1019  
 Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met  
 305 310 315 320

gaa atg gat cgt tgt ggg gac aac aat gag ctg gct tgg aac ttc tgt 1067  
 Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys  
 325 330 335

atg atg gat aca ggg ttt tct ccg ttt ttg act gat cag aat ctc gcg 1115  
 Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala  
 340 345 350

aat gag aat ccc ata gag tat ccg gag cta ttc aat gag tta gca ttt 1163  
 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe  
 355 360 365

gag gac aac atc gac ttc atg ttc gat gat ggg aag cac gag tgc ttg 1211  
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu  
 370 375 380

aac ttg gaa aat ctg gat tgt tgc gtg gtg gga aga gag agc cca ccc 1259  
 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro  
 385 390 395 400

tct tct tct tca cca ttg tct tgc tta tct act gac tct gct tca tca 1307  
 Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser  
 405 410 415

aca aca aca aca aca acc tcg gtt tct tgt aac tat ttg gtc 1349  
 Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val  
 420 425 430

tgagagagag agctttgcct tctagtttga atttctatatt cttccgcttc ttcttctttt 1409  
 ttttctttttg ttgggttctg cttagggttt gtatttcagt ttcagggtt gttcgttggt 1469  
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 a 1530

&lt;210&gt; 34

&lt;211&gt; 430

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

<223> G979

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20 25 30

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly  
35 40 45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser  
50 55 60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala  
65 70 75 80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly  
85 90 95

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His  
100 105 110

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu  
115 120 125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg  
130 135 140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly  
145 150 155 160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His  
165 170 175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr  
180 185 190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr  
195 200 205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe  
210 215 220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro  
225 230 235 240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala  
245 250 255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu  
260 265 270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys  
275 280 285

Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser  
 290 295 300  
 Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met  
 305 310 315 320  
 Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys  
 325 330 335  
 Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala  
 340 345 350  
 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe  
 355 360 365  
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu  
 370 375 380  
 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro  
 385 390 395 400  
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 405 410 415  
 Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val  
 420 425 430

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 <212> DNA  
 <213> Arabidopsis thaliana

<220>  
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 <222> (6)..(1088)  
 <223> G993

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ctc tcc atc tct act act cca aag ccg aca acg acg acg gag aag aaa 98  
 Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys  
 20 25 30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc 146  
 Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser  
 35 40 45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag 194  
 Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu  
 50 55 60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242  
 Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro  
 65 70 75



aac Asn 80	gga Gly	aga Arg	tgg Trp	gga Gly	gct Ala 85	cag Gln	att Ile	tac Tyr	gag Glu	aag Lys 90	cat His	cag Gln	cga Arg	gtt Val	tgg Trp 95	290
ctc Leu	ggt Gly	act Thr	ttc Phe	aac Asn 100	gag Glu	gaa Glu	gaa Glu	gaa Glu	gct Ala 105	gcg Ala	tct Ser	tct Ser	tac Tyr	gac Asp 110	atc Ile	338
gcc Ala	gtg Val	agg Arg	aga Arg 115	ttc Phe	cgc Arg	ggc Gly	cgc Arg	gac Asp 120	gcc Ala	gtc Val	act Thr	aac Asn	ttc Phe	aaa Lys	tct Ser	386
caa Gln	gtt Val	gat Asp 130	gga Gly	aac Asn	gac Asp	gcc Ala	gaa Glu 135	tcg Ser	gct Ala	ttt Phe	ctt Leu	gac Asp 140	gct Ala	cat His	tct Ser	434
aaa Lys 145	gct Ala	gag Glu	atc Ile	gtg Val	gat Asp	atg Met 150	ttg Leu	agg Arg	aaa Lys	cac His	act Thr 155	tac Tyr	gcc Ala	gat Asp	gag Glu	482
ttt Phe 160	gag Glu	cag Gln	agt Ser	aga Arg	cgg Arg 165	aag Lys	ttt Phe	gtt Val	aac Asn	ggc Gly 170	gac Asp	gga Gly	aaa Lys	cgc Arg	tct Ser 175	530
ggg Gly	ttg Leu	gag Glu	acg Thr	gcg Ala 180	acg Thr	tac Tyr	gga Gly	aac Asn	gac Asp 185	gct Ala	gtt Val	ttg Leu	aga Arg	gcg Ala 190	cgt Arg	578
gag Glu	gtt Val	ttg Leu	ttc Phe 195	gag Glu	aag Lys	act Thr	gtt Val	acg Thr 200	ccg Pro	agc Ser	gac Asp	gtc Val	ggg Gly 205	aag Lys	ctg Leu	626
aac Asn 210	cgt Arg	tta Leu	gtg Val	ata Ile	ccg Pro	aaa Lys	caa Gln 215	cac His	gcg Ala	gag Glu	aag Lys	cat His 220	ttt Phe	ccg Pro	tta Leu	674
ccg Pro 225	gcg Ala	atg Met	acg Thr	acg Thr	gcg Ala	atg Met 230	ggg Gly	atg Met	aat Asn	ccg Pro	tct Ser 235	ccg Pro	acg Thr	aaa Lys	ggc Gly	722
gtt Val 240	ttg Leu	att Ile	aac Asn	ttg Leu	gaa Glu 245	gat Asp	aga Arg	aca Thr	ggg Gly	aaa Lys 250	gtg Val	tgg Trp	cgg Arg	ttc Phe	cgt Arg 255	770
tac Tyr	agt Ser	tac Tyr	tgg Trp	aac Asn 260	agc Ser	agt Ser	caa Gln	agt Ser	tac Tyr 265	gtg Val	ttg Leu	acc Thr	aag Lys	ggc Gly 270	tgg Trp	818
agc Ser	cgg Arg	ttc Phe	gtt Val	aaa Lys 275	gag Glu	aag Lys	aat Asn	ctt Leu 280	cga Arg	gcc Ala	ggg Gly	gat Asp	gtg Val	gtt Val	tgt Cys	866
ttc Phe	gag Glu	aga Arg	tca Ser	acc Thr	gga Gly	cca Pro	gac Asp 295	cgg Arg	caa Gln	ttg Leu	tat Tyr	atc Ile	cac His	tgg Trp	aaa Lys	914

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gtc  cgg  tct  agt  ccg  gtt  cag  act  gtg  gtt  agg  cta  ttc  gga  gtc  aac  962
Val  Arg  Ser  Ser  Pro  Val  Gln  Thr  Val  Val  Arg  Leu  Phe  Gly  Val  Asn
      305                      310                      315

att  ttc  aat  gtg  agt  aac  gag  aaa  cca  aac  gac  gtc  gca  gta  gag  tgt  1010
Ile  Phe  Asn  Val  Ser  Asn  Glu  Lys  Pro  Asn  Asp  Val  Ala  Val  Glu  Cys
320                      325                      330                      335

gtt  ggc  aag  aag  aga  tct  cgg  gaa  gat  gat  ttg  ttt  tcg  tta  ggg  tgt  1058
Val  Gly  Lys  Lys  Arg  Ser  Arg  Glu  Asp  Asp  Leu  Phe  Ser  Leu  Gly  Cys
      340                      345                      350

tcc  aag  aag  cag  gcg  att  atc  aac  atc  ttg  tgacaaattc  tttttttttg  1108
Ser  Lys  Lys  Gln  Ala  Ile  Ile  Asn  Ile  Leu
      355                      360

gttttttttct  tcaatttggt  tctccttttt  caatatatttg  tattgaaatg  acaagttgta 1168

aattaggaca  agacaagaaa  aaatgacaac  tagacaaaat  agttttttggt  taaaaaaaaa 1228

aaaaaaaaaaa a 1239

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<211> 361
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G993

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      20          25          30

Ser  Ser  Pro  Pro  Ala  Thr  Ser  Met  Arg  Leu  Tyr  Arg  Met  Gly  Ser  Gly
      35          40          45

Gly  Ser  Ser  Val  Val  Leu  Asp  Ser  Glu  Asn  Gly  Val  Glu  Thr  Glu  Ser
      50          55          60

Arg  Lys  Leu  Pro  Ser  Ser  Lys  Tyr  Lys  Gly  Val  Val  Pro  Gln  Pro  Asn
      65          70          75          80

Gly  Arg  Trp  Gly  Ala  Gln  Ile  Tyr  Glu  Lys  His  Gln  Arg  Val  Trp  Leu
      85          90          95

Gly  Thr  Phe  Asn  Glu  Glu  Glu  Glu  Ala  Ala  Ser  Ser  Tyr  Asp  Ile  Ala
      100          105          110

Val  Arg  Arg  Phe  Arg  Gly  Arg  Asp  Ala  Val  Thr  Asn  Phe  Lys  Ser  Gln
      115          120          125

Val  Asp  Gly  Asn  Asp  Ala  Glu  Ser  Ala  Phe  Leu  Asp  Ala  His  Ser  Lys
      130          135          140

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Lys Lys Gln Ala Ile Ile Asn Ile Leu  
355 360

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<400> 37
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ttctactttt tctcgttacc acaaaactct ttcaccgata ttctcgttcc attcttcttc 120
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ctaattacac c atg ccc aac atc acc atg ggt ttg aaa ccc gac ccg gtt 170  
 Met Pro Asn Ile Thr Met Gly Leu Lys Pro Asp Pro Val  
 1 5 10

gct cca acg aac ccg act cat cat gag agt aat gct gcc aaa gag att 218  
 Ala Pro Thr Asn Pro Thr His His Glu Ser Asn Ala Ala Lys Glu Ile  
 15 20 25

cgt tac aga ggc gtt agg aaa cgt cca tgg gga aga tac gcc gct gag 266  
 Arg Tyr Arg Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu  
 30 35 40 45

atc cga gat ccg gtt aag aaa act cga gtc tgg ctc ggt acg ttc gac 314  
 Ile Arg Asp Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp  
 50 55 60

acc gct cag cag gcg gcg cgt gct tac gac gca gcc gcg cgt gac ttt 362  
 Thr Ala Gln Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe  
 65 70 75

cgt ggt gtt aag gct aag acc aat ttc ggt gtt atc gtt ggt agt agt 410  
 Arg Gly Val Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser  
 80 85 90

cct act cag agt agc acc gtc gtc gac tct ccc acg gcg gca ccg ttt 458  
 Pro Thr Gln Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe  
 95 100 105

ata aca cct ccg cac ctc gag ctc agc tta ggc ggc ggc ggc gcg tgt 506  
 Ile Thr Pro Pro His Leu Glu Leu Ser Leu Gly Gly Gly Gly Ala Cys  
 110 115 120 125

cgt cgt aag atc ccg ctt gtg cat ccg gtt tac tac tat aac atg gcg 554  
 Arg Arg Lys Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala  
 130 135 140

acg tat cca aag atg acg acg tgt ggt gtc cag agc gag tct gaa acg 602  
 Thr Tyr Pro Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr  
 145 150 155

tcg tcg gtc gtt gat ttc gaa ggt gga gct ggg aag ata tct ccg ccg 650  
 Ser Ser Val Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro  
 160 165 170

tta gat ctg gat ctt aac tta gct cct ccg gcg gaa taggccgtga 696  
 Leu Asp Leu Asp Leu Asn Leu Ala Pro Pro Ala Glu  
 175 180 185

gttttttttt tcttatgtcg tttctttaga caaaaaaaaaa taacgtttcc tttttttttc 756

tgcctaagaa aaaaatatta tccgtttttt agaagaaaaa aaaaaaaaaa aaaaaaa 813

&lt;210&gt; 38

&lt;211&gt; 185

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

0034510-091300

&lt;220&gt;

&lt;223&gt; G1020

&lt;400&gt; 38

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 20 25 30

Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp  
 35 40 45

Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Gln  
 50 55 60

Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe Arg Gly Val  
 65 70 75 80

Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser Pro Thr Gln  
 85 90 95

Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe Ile Thr Pro  
 100 105 110

Pro His Leu Glu Leu Ser Leu Gly Gly Gly Gly Ala Cys Arg Arg Lys  
 115 120 125

Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala Thr Tyr Pro  
 130 135 140

Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr Ser Ser Val  
 145 150 155 160

Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro Leu Asp Leu  
 165 170 175

Asp Leu Asn Leu Ala Pro Pro Ala Glu  
 180 185

&lt;210&gt; 39

&lt;211&gt; 1693

&lt;212&gt; DNA

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (252)..(1247)

&lt;223&gt; G1023

&lt;220&gt;

<223> "n" at various positions throughout the sequence  
 may be A, T, C, G, other or unknown

&lt;400&gt; 39

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0034510-09136600

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cttgttcttg	ggtaaaggac	ttttcttggt	cttgagagag	ttcattttga	ggcttttctg	180										
ggaattttga	gaggtttttt	aggggttaag	ggggtttggt	tttgaatttc	gcacaccaag	240										
tgttcgataa	a	atg	gct	gaa	cga	aag	aaa	cgc	tct	tct	att	caa	acc	aat	290	
	Met	Ala	Glu	Arg	Lys	Lys	Arg	Ser	Ser	Ile	Gln	Thr	Asn			
	1					5					10					
aaa	ccc	aac	aaa	aaa	ccc	atg	aag	aag	aaa	cct	ttt	cag	cta	aat	cac	338
Lys	Pro	Asn	Lys	Lys	Pro	Met	Lys	Lys	Lys	Pro	Phe	Gln	Leu	Asn	His	
	15					20					25					
ctc	cca	ggg	tta	tct	gaa	gat	ttg	aag	act	atg	aga	aaa	ctc	cgt	ttc	386
Leu	Pro	Gly	Leu	Ser	Glu	Asp	Leu	Lys	Thr	Met	Arg	Lys	Leu	Arg	Phe	
	30				35					40					45	
gtt	gtg	aat	gat	cct	tac	gct	act	gac	tac	tca	tca	agc	gaa	gaa	gaa	434
Val	Val	Asn	Asp	Pro	Tyr	Ala	Thr	Asp	Tyr	Ser	Ser	Ser	Glu	Glu	Glu	
				50					55					60		
gaa	agg	agt	cag	aga	agg	aaa	cgt	tat	gtc	tgt	gag	atc	gat	ctt	cct	482
Glu	Arg	Ser	Gln	Arg	Arg	Lys	Arg	Tyr	Val	Cys	Glu	Ile	Asp	Leu	Pro	
			65					70					75			
ttc	gct	caa	gct	gct	act	caa	gca	gaa	tct	gaa	agc	tca	tat	tgt	cag	530
Phe	Ala		Gln	Ala	Ala	Thr	Gln	Ala	Glu	Ser	Glu	Ser		Tyr	Cys	Gln
		80						85					90			
gag	agt	aac	aat	aat	ggg	gta	agc	aag	act	aaa	atc	tca	gct	tgt	agc	578
Glu	Ser	Asn	Asn	Asn	Gly	Val	Ser	Lys	Thr	Lys	Ile	Ser	Ala	Cys	Ser	
	95					100					105					
aaa	aag	gtt	tta	cgc	agc	aaa	gca	tct	ccg	gtc	gtt	gga	cgt	tct	tct	626
Lys	Lys	Val	Leu	Arg	Ser	Lys	Ala	Ser	Pro	Val	Val	Gly	Arg	Ser	Ser	
110					115					120					125	
act	act	gtc	tcg	aag	cct	gtt	ggg	gtt	agg	cag	agg	aaa	tgg	ggg	aaa	674
Thr	Thr	Val	Ser	Lys	Pro	Val	Gly	Val	Arg	Gln	Arg	Lys	Trp	Gly	Lys	
				130					135					140		
tgg	gct	gct	gag	att	aga	cat	cca	atc	acc	aaa	gta	aga	act	tgg	ttg	722
Trp	Ala	Ala	Glu	Ile	Arg	His	Pro	Ile	Thr	Lys	Val	Arg	Thr	Trp	Leu	
			145					150					155			
ggg	act	tac	gag	acg	ctt	gaa	caa	gca	gct	gat	gct	tat	gct	acc	aag	770
Gly	Thr	Tyr	Glu	Thr	Leu	Glu	Gln	Ala	Ala	Asp	Ala	Tyr	Ala	Thr	Lys	
		160					165					170				
aag	ctt	gag	ttt	gat	gct	ctg	gct	gca	gcc	act	tct	gct	gct	tcc	tct	818
Lys	Leu	Glu	Phe	Asp	Ala	Leu	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Ser	Ser	
	175					180					185					
gtt	ttg	tca	aat	gag	tct	ggg	tct	atg	atc	tca	gcc	tca	ggg	tca	agc	866
Val	Leu	Ser	Asn	Glu	Ser	Gly	Ser	Met	Ile	Ser	Ala	Ser	Gly	Ser	Ser	
190																

att gat ctt gac aag aag cta gtt gat tcg act ctt gat caa caa gct 914  
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 Gly Glu Ser Lys Lys Ala Ser Phe Asp Phe Asp Phe Ala Asp Leu Gln  
 225 230 235

att cct gaa atg ggt tgc ttc att gat gac tca ttc atc cca aat gct 1010  
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 240 245 250

tgt gag ctt gat ttt ctc tta aca gaa gag aac aac aac caa atg ttg 1058  
 Cys Glu Leu Asp Phe Leu Leu Thr Glu Glu Asn Asn Asn Gln Met Leu  
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gat gat tac tgt ggc ata gat gat ctg gac atc att ggt ctt gaa tgt 1106  
 Asp Asp Tyr Cys Gly Ile Asp Asp Leu Asp Ile Ile Gly Leu Glu Cys  
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gac ggt cca agc gaa ctt cca gac tat gat ttc tca gat gtg gag atc 1154  
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cat atc gca aca act act ccc act cct ctt aat atc gcg tgc cca 1247  
 His Ile Ala Thr Thr Thr Pro Thr Pro Leu Asn Ile Ala Cys Pro  
 320 325 330

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Asp	Pro	Tyr	Ala	Thr	Asp	Tyr	Ser	Ser	Ser	Glu	Glu	Glu	Glu	Arg	Ser
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Ala	Ala	Thr	Gln	Ala	Glu	Ser	Glu	Ser	Ser	Tyr	Cys	Gln	Glu	Ser	Asn
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Leu	Arg	Ser	Lys	Ala	Ser	Pro	Val	Val	Gly	Arg	Ser	Ser	Thr	Thr	Val
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Ser	Lys	Pro	Val	Gly	Val	Arg	Gln	Arg	Lys	Trp	Gly	Lys	Trp	Ala	Ala
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Glu	Thr	Leu	Glu	Gln	Ala	Ala	Asp	Ala	Tyr	Ala	Thr	Lys	Lys	Leu	Glu
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Phe	Asp	Ala	Leu	Ala	Ala	Ala	Thr	Ser	Ala	Ala	Ser	Ser	Val	Leu	Ser
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Asn	Glu	Ser	Gly	Ser	Met	Ile	Ser	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Leu
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Asp	Lys	Lys	Leu	Val	Asp	Ser	Thr	Leu	Asp	Gln	Gln	Ala	Gly	Glu	Ser
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Lys	Lys	Ala	Ser	Phe	Asp	Phe	Asp	Phe	Ala	Asp	Leu	Gln	Ile	Pro	Glu
225					230					235					240
Met	Gly	Cys	Phe	Ile	Asp	Asp	Ser	Phe	Ile	Pro	Asn	Ala	Cys	Glu	Leu
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Asp	Phe	Leu	Leu	Thr	Glu	Glu	Asn	Asn	Asn	Gln	Met	Leu	Asp	Asp	Tyr
			260					265					270		
Cys	Gly	Ile	Asp	Asp	Leu	Asp	Ile	Ile	Gly	Leu	Glu	Cys	Asp	Gly	Pro
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Ser	Glu	Leu	Pro	Asp	Tyr	Asp	Phe	Ser	Asp	Val	Glu	Ile	Asp	Leu	Gly
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00394519-093660



Leu Ile Gly Thr Thr Ile Asp Lys Tyr Ala Phe Val Asp His Ile Ala  
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gacaattata acagtataga gaaggaagaa agaaaagaaa aagaaaccgt tgttgattta 180  
gatacagaga agagaagatc atctaac atg gga aga tct cct atc tct gat gac 234  
Met Gly Arg Ser Pro Ile Ser Asp Asp  
1 5  
tct ggt ctc aag aaa ggt cct tgg act cct gat gaa gat gag aaa ctt 282  
Ser Gly Leu Lys Lys Gly Pro Trp Thr Pro Asp Glu Asp Glu Lys Leu  
10 15 20 25  
gtc aac tat gtt caa aaa cat ggt cat agt agc tgg aga gcc ctt ccc 330  
Val Asn Tyr Val Gln Lys His Gly His Ser Ser Trp Arg Ala Leu Pro  
30 35 40  
aaa ctc gct ggt ctt aac agg tgt ggg aag agt tgc agg cta aga tgg 378  
Lys Leu Ala Gly Leu Asn Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp  
45 50 55  
acg aac tac ttg aga cca gac atc aag aga ggg aga ttc tct ccg gac 426  
Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Pro Asp  
60 65 70  
gag gaa cag act atc ttg aat ctt cat tca gtt ctt gga aac aag tgg 474  
Glu Glu Gln Thr Ile Leu Asn Leu His Ser Val Leu Gly Asn Lys Trp  
75 80 85  
tca acg att gcg aat cag tta cca ggg aga aca gat aac gag atc aag 522  
Ser Thr Ile Ala Asn Gln Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys  
90 95 100 105  
aat ttc tgg aac act cat ttg aag aag aag ctg att cag atg ggt ttt 570  
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Gly	His	Ser 35	Ser	Trp	Arg	Ala	Leu 40	Pro	Lys	Leu	Ala	Gly 45	Leu	Asn	Arg
Cys	Gly 50	Lys	Ser	Cys	Arg	Leu 55	Arg	Trp	Thr	Asn	Tyr 60	Leu	Arg	Pro	Asp
Ile 65	Lys	Arg	Gly	Arg	Phe 70	Ser	Pro	Asp	Glu	Glu 75	Gln	Thr	Ile	Leu	Asn 80
Leu	His	Ser	Val	Leu 85	Gly	Asn	Lys	Trp	Ser 90	Thr	Ile	Ala	Asn	Gln 95	Leu
Pro	Gly	Arg	Thr 100	Asp	Asn	Glu	Ile	Lys 105	Asn	Phe	Trp	Asn	Thr 110	His	Leu
Lys	Lys	Lys 115	Leu	Ile	Gln	Met	Gly 120	Phe	Asp	Pro	Met	Thr 125	His	Arg	Pro
Arg	Thr 130	Asp	Ile	Phe	Ser	Gly 135	Leu	Ser	Gln	Leu	Met 140	Ser	Leu	Ser	Ser
Asn 145	Leu	Arg	Gly	Phe	Val 150	Asp	Leu	Gln	Gln	Gln 155	Phe	Pro	Ile	Asp	Gln 160
Glu	His	Thr	Ile 165	Leu	Lys	Leu	Gln	Thr	Glu 170	Met	Ala	Lys	Leu	Gln 175	Leu
Phe	Gln	Tyr	Leu 180	Leu	Gln	Pro	Ser	Ser 185	Met	Ser	Asn	Asn	Val 190	Asn	Pro
Asn	Asp	Phe 195	Asp	Thr	Leu	Ser	Leu 200	Leu	Asn	Ser	Ile	Ala 205	Ser	Phe	Lys
Glu	Thr 210	Ser	Asn	Asn	Thr	Thr 215	Ser	Asn	Asn	Leu	Asp 220	Leu	Gly	Phe	Leu

Gly Ser Tyr Leu Gln Asp Phe His Ser Leu Pro Ser Leu Lys Thr Leu  
 225 230 235 240  
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 245 250 255  
 Asn His Phe Lys Phe Ser Thr Gln Arg Glu Asn Leu Pro Val Ser Pro  
 260 265 270  
 Ile Trp Leu Ser Asp Pro Ser Ser Thr Thr Pro Ala His Val Asn Asp  
 275 280 285  
 Asp Leu Ile Phe Asn Gln Tyr Gly Ile Glu Asp Val Asn Ser Asn Ile  
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 Met Glu Gly Ser Ser Lys  
 1 5  
 ggg ttg agg aaa ggt gca tgg act gct gaa gaa gat agt ctc ttg agg 161  
 Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp Ser Leu Leu Arg  
 10 15 20  
 cta tgt att gat aag tat gga gaa ggc aaa tgg cat caa gtt cct ttg 209  
 Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His Gln Val Pro Leu  
 25 30 35  
 aga gct ggg cta aat cga tgc aga aag agt tgt aga cta aga tgg ttg 257  
 Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg Leu Arg Trp Leu  
 40 45 50  
 aac tat ttg aag cca agt atc aag aga gga aga ctt agc aat gat gaa 305  
 Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu Ser Asn Asp Glu  
 55 60 65 70  
 gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga aat agg tgg tcc 353  
 Val Asp Leu Leu Leu Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser  
 75 80 85

66660:6454660

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                   90                                  95                                  100

tac tgg aac acc cat ctg agt aaa aaa cat gag tct tcg tgt tgt aag 449  
 Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser Ser Cys Cys Lys  
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tct aaa atg aaa aag aaa aac att att tcc cct cct aca aca ccg gtc 497  
 Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro Thr Thr Pro Val  
                   120                                  125                                  130

caa aaa atc ggt gtt ttt aag cct cga cct cga tcc ttc tct gtt aac 545  
 Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser Phe Ser Val Asn  
                   135                                  140                                  145                                  150

aat ggt tgc agc cat ctc aat ggt ctg cca gaa gtt gat tta att cct 593  
 Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val Asp Leu Ile Pro  
                                   155                                  160                                  165

tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa aat agt atc aca 641  
 Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu Asn Ser Ile Thr  
                                   170                                  175                                  180

tgt aac aaa gat gat gag aaa gat gat ttt gtg aat aat cta atg aat 689  
 Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn Asn Leu Met Asn  
                   185                                  190                                  195

gga gat aat atg tgg ttg gag aat tta ctg ggg gaa aac caa gaa gct 737  
 Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu Asn Gln Glu Ala  
                   200                                  205                                  210

gat gcg att gtt cct gaa gcg acg aca gct gaa cat ggg gcc act ttg 785  
 Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His Gly Ala Thr Leu  
                   215                                  220                                  225                                  230

gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat gga gag act gtt 833  
 Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp Gly Glu Thr Val  
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gaa ctt gat tagtggttct caccgtttgt ttaagattgt ggggtggcttt 882  
 Glu Leu Asp

tctttcgtat tttagtaatg tatttttctg tatgaagtaa agaatttcag cattttaaga 942

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&lt;223&gt; G664

&lt;400&gt; 45

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ccg tgc tgt gag aaa gct cac aca aac aaa gga gca tgg acg aaa gaa 163
Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala Trp Thr Lys Glu
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gag gac gag agg ctc gtc gcc tac att aaa gct cat gga gaa ggc tgc 211
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tgg aga tct ctc ccc aaa gcc gcc gga ctt ctt cgc tgt ggc aag agc 259
Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg Cys Gly Lys Ser
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tgc cgt ctc cgg tgg atc aac tat ctc cgg cct gac ctt aag cgt gga 307
Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly
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aac ttc acc gag gaa gaa gac gaa ctc atc atc aag ctc cat agc ctt 355
Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu
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ctt ggc aac aaa tgg tcg ctt att gcc ggg aga tta ccg gga aga aca 403
Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
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gat aac gag ata aag aac tat tgg aac acg cat ata cga aga aag ctt 451
Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile Arg Arg Lys Leu
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ata aac aga ggg att gat cca acg agt cat aga cca atc caa gaa tca 499
Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro Ile Gln Glu Ser
                120                      125                      130

tca gct tct caa gat tct aaa cct aca caa cta gaa cca gtt acg agt 547
Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu Pro Val Thr Ser
                135                      140                      145

aat acc att aat atc tca ttc act tct gct cca aag gtc gaa acg ttc 595
Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys Val Glu Thr Phe
                150                      155                      160

cat gaa agt ata agc ttt ccg gga aaa tca gag aaa atc tca atg ctt 643
His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys Ile Ser Met Leu
165                      170                      175                      180

acg ttc aaa gaa gaa aaa gat gag tgc cca gtt caa gaa aag ttc cca 691
Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln Glu Lys Phe Pro
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66460"6454660

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 200 205 210

ctt caa ggg cat gga aag tca aca acg cca cgt tgt ttc aag tgc agc 787  
 Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys Phe Lys Cys Ser  
 215 220 225

tta ggg atg ata aac ggc atg gag tgc aga tgc gga aga atg aga tgc 835  
 Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Cys  
 230 235 240

gat gta gtc gga ggt agc agc aag ggg agt gac atg agc aat gga ttt 883  
 Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn Gly Phe  
 245 250 255 260

gat ttt tta ggg ttg gca aag aaa gag acc act tct ctt ttg ggc ttt 931  
 Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu Leu Gly Phe  
 265 270 275

cga agc ttg gag atg aaataatatt gtcaaatttt aggcgtaact gtacaaaact 986  
 Arg Ser Leu Glu Met  
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 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp  
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 Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys  
 65 70 75 80  
 Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu  
 85 90 95  
 Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile  
 100 105 110

66160-6154650



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 115 120 125  
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 130 135 140  
 Pro Val Thr Ser Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys  
 145 150 155 160  
 Val Glu Thr Phe His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys  
 165 170 175  
 Ile Ser Met Leu Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln  
 180 185 190  
 Glu Lys Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp  
 195 200 205  
 Asp Val Asp Arg Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys  
 210 215 220  
 Phe Lys Cys Ser Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly  
 225 230 235 240  
 Arg Met Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met  
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 Met Thr Arg Arg Cys Ser His Cys Asn His Asn Gly His Asn Ser  
 1 5 10 15  
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Ser Pro Gly Asp Val Pro Asp His Val Ala Gly Asp Gly Tyr Ala Ser	
65 70 75	
gag gat ttc gtt gct ggc tct tcc tct agc cgc gag aga aag aaa gga	408
Glu Asp Phe Val Ala Gly Ser Ser Ser Ser Arg Glu Arg Lys Lys Gly	
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Thr Pro Trp Thr Glu Glu Glu His Arg Met Phe Leu Leu Gly Leu Gln	
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Lys Leu Gly Lys Gly Asp Trp Arg Gly Ile Ser Arg Asn Tyr Val Thr	
115 120 125	
act agg aca cct aca caa gtt gct agc cat gct cag aag tat ttc atc	552
Thr Arg Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile	
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Arg Gln Ser Asn Val Ser Arg Arg Lys Arg Arg Ser Ser Leu Phe Asp	
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Met Val Pro Asp Glu Val Gly Asp Ile Pro Met Asp Leu Gln Glu Pro	
160 165 170 175	
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Glu Glu Asp Asn Ile Pro Val Glu Thr Glu Met Gln Gly Ala Asp Ser	
180 185 190	
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Ile His Gln Thr Leu Ala Pro Ser Ser Leu His Ala Pro Ser Ile Leu	
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Glu Pro Thr Ala Thr Ala Ala Ala Ser Ser Ser Ser Arg Leu Glu	
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Glu Thr Thr Gln Leu Gln Ser Gln Leu Gln Pro Gln Pro Gln Leu Pro	
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 Gly Ser Phe Pro Ile Leu Tyr Pro Thr Tyr Phe Ser Pro Tyr Tyr Pro  
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 Phe Pro Phe Pro Ile Trp Pro Ala Gly Tyr Val Pro Glu Pro Pro Lys  
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 Lys Glu Glu Thr His Glu Ile Leu Arg Pro Thr Ala Val His Ser Lys  
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 65 70 75 80

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 Thr Val Ile Gln Ile Arg Ser His Ala Gln Lys Tyr Phe Leu Lys Val  
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agt	agt	att	ctc	gat	atc	gat	cag	cac	cat	gcc	atg	aac	ctc	tta	aac		623
Ser	Ser	Ile	Leu	Asp	Ile	Asp	Gln	His	His	Ala	Met						



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Gly Tyr Ala Ser Ala Asn Asp Ala Val Gln Ile Ser Ser Ser Ser Gly  
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Gly Arg Lys Arg Gly Val Pro Trp Thr Glu Asn Glu His Lys Arg Phe  
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 Ser Ser Leu Phe Asp Ile Thr Thr Glu Thr Val Thr Glu Met Ala Met  
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662160-1515150



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gac Asp	gga Gly 270	gaa Glu	ggg Gly	att Ile	gac Asp	cat His 275	tct Ser	ttg Leu	ttc Phe	agc Ser	ttc Phe 280	aac Asn	tcc Ser	ata Ile	gat Asp	1046

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 Val Leu Phe  
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Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly  
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Ile Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Met Ile Leu His  
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu  
 85 90 95

Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu  
 100 105 110

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Lys Lys Lys Leu Lys Lys Met Asn Asp Ser Cys Asp Ser Thr Ile Asn  
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 Asn Gly Leu Asp Asn Lys Asp Phe Ser Ile Ser Asn Lys Asn Thr Thr  
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 Ser His Gln Ser Ser Asn Ser Ser Lys Gly Gln Trp Glu Arg Arg Leu  
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 Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Cys Asp Ala Leu Ser  
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 Ile Asp Lys Pro Gln Asn Pro Thr Asn Phe Ser Ile Pro Asp Leu Gly  
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 Tyr Gly Pro Ser Ser Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr  
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 may be A, T, C, G, other or unknown

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Pro	Trp	Thr	Val	Glu	Glu	Asp	Gly	Lys	Leu	Val	Asp	Phe	Leu	Arg	Ala	
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Trp	Thr	Asn	Tyr	Leu	Arg	Pro	Asp	Leu	Lys	Arg	Gly	Leu	Phe	Thr	Glu	
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Lys	Asn	Tyr	Trp	Asn	Thr	His	Ile	Lys	Arg	Lys	Leu	Ile	Arg	Met	Gly	
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Glu	Glu	Thr	Ile	Leu	Val	Asn	Asp	Pro	Lys	Pro	Leu	Ser	Glu	Thr	Glu	
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Leu	Asn	Gln	Leu	Ala	Asp	Val	Asp	Gly	Asp	Asp	Gln	Pro	Trp	Ser	Phe	
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cta	atg	gaa	aat	gac	gaa	gga	gga	ggt	ggc	gac	gcc	gcc	gga	gag	ctt	803
Leu	Met	Glu	Asn	Asp	Glu	Gly	Gly	Gly	Gly	Asp	Ala	Ala	Gly	Glu	Leu	
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Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu
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Gly Cys Phe Asp Val
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Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg
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Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu
      65                70                75                80

Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
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Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
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Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
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Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
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atg gga aga cat tca tgt tgt tac aaa cag aaa ctg agg aaa gga ctt 166
Met Gly Arg His Ser Cys Cys Tyr Lys Gln Lys Leu Arg Lys Gly Leu
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Trp Ser Pro Glu Glu Asp Glu Lys Leu Leu Arg Tyr Ile Thr Lys Tyr
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Gly His Gly Cys Trp Ser Ser Val Pro Lys Gln Ala Gly Leu Gln Arg
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Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
      50             55             60
ttg aag aga gga gca ttt tct caa gat gaa gaa aat ctc att att gaa 358
Leu Lys Arg Gly Ala Phe Ser Gln Asp Glu Glu Asn Leu Ile Ile Glu
      65             70             75             80
ctt cat gcc gtt ctt ggc aat aga tgg tct cag ata gct gca cag ctt 406
Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Gln Leu
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50 55 60

Leu Lys Arg Gly Ala Phe Ser Gln Asp Glu Glu Asn Leu Ile Ile Glu  
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Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Cys Leu  
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Lys Lys Lys Leu Arg Leu Arg Gly Ile Asp Pro Val Thr His Lys Leu  
115 120 125

Leu Thr Glu Ile Glu Thr Gly Thr Asp Asp Lys Thr Lys Pro Val Glu  
130 135 140

Lys Ser Gln Gln Thr Tyr Leu Val Glu Thr Asp Gly Ser Ser Ser Thr  
145 150 155 160

Thr Thr Cys Ser Thr Asn Gln Asn Asn Asn Thr Asp His Leu Tyr Thr  
165 170 175

Gly Asn Phe Gly Phe Gln Arg Leu Ser Leu Glu Asn Gly Ser Arg Ile  
180 185 190

Ala Ala Gly Ser Asp Leu Gly Ile Trp Ile Pro Gln Thr Gly Arg Asn  
195 200 205

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Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile
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Ile	Ile	Gln	Leu	His	Ser	Ile	Met	Gly	Asn	Lys	Trp	Ser	Ala	Ile	Ala	
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Ala	Arg	Leu	Pro	Gly	Arg	Thr	Asp	Asn	Glu	Ile	Lys	Asn	Tyr	Trp	Asn	
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 Ser Val Thr Ala Ile Asp Ala Gly Met Val Lys Glu Glu Gln Asn Asn  
 260 265 270  
  
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 Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly Glu  
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 Phe Ile Asp Asn Asp Asp Gln Phe Ser Ser Phe Phe Asp Ser Tyr Cys  
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Cys Thr His Lys Pro Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln  
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210 215 220

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Ser Ser Val Thr Ala Ile Asp Ala Gly Met Val Lys Glu Glu Gln Asn  
260 265 270

Asn Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly  
275 280 285

Glu Asp Leu Ser Leu Val Trp Gln Glu Thr Met Met Phe Asp Asp His  
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Gln Asn His Tyr Tyr Cys Gly Glu Thr Ser Thr Thr Ser His Gln Phe  
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Asp Gln Tyr Ser Ser Ser Leu Val Asp Thr Ser Leu Asp Leu Thr Ile  
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Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu  
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Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser Cys	
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gcg gtt att ggc gga gtg tcg gag agt agc tca acg gat caa gat gag	454
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Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys Val	
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Ser Arg Val Tyr Tyr Lys Thr Glu Ala Ser Asp Thr Thr Leu Val Val	
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Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser	
245 250 255	
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Ala Ser Ala Ser Lys Val Val Glu Lys Lys Trp Leu Val Lys Asp Glu  
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aag aga aat atg cta caa gat gaa ata aac cgg gtt aat tcg gag aac 198  
Lys Arg Asn Met Leu Gln Asp Glu Ile Asn Arg Val Asn Ser Glu Asn  
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aag aag cta acc gaa atg tta gca aga gtc tgt gag aag tac tat gct 246  
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Lys Tyr Tyr Ala  
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Asn	Ile	Thr	Asn	Asp	Lys	Ala	Thr	Val	Ser	Thr	Ala	Tyr	Phe	Ala	Ala	
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115	120	125
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Lys Glu Leu Glu Tyr Cys Asn Ile Glu Ser Glu Asn Phe Val Pro Cys	
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Phe Asn Val Ser Glu Asn Leu Ala Leu Gly Tyr Ser Asn Gly Asp Glu	
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Asn Asp Arg Phe Cys Gly Pro Gly Ser Lys Gln Glu Cys Leu Glu Leu	
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Pro Pro Val Lys Tyr Arg Val Pro Leu Arg Trp Pro Thr Gly Lys Asp	
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Ile Ile Trp His Ser Asn Val Lys Ile Thr Ala Gln Glu Val Val Ser	
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Ser Gly Ser Ile Thr Lys Arg Met Met Met Met Glu Asp Asp Gln Ile	
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Ser Phe Arg Ser Ala Ser Pro Met Ser Asp Glu Val Glu Asp Tyr Ser	
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Tyr Glu Ala Ser Gly Ser Gln Val Gln Leu Thr Leu Glu Arg Gly Leu	
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Pro Ala Met Ile Gly Ser Phe Ile Ser Lys Gln Leu Pro Tyr Pro Ser	
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Leu Ser Phe Asp Met Leu His Cys Leu Arg Cys Gly Ile Asp Trp Asp	
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Gln Lys Asp Gly Leu Leu Leu Val Glu Ile Asp Arg Val Leu Lys Pro	
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ggg Gly	ggg Gly	tac Tyr 370	ttt Phe	gta Val	tgg Trp	aca Thr	tct Ser 375	ccg Pro	ctc Leu	aca Thr	aac Asn	cct Pro 380	cgt Arg	aac Asn	aag Lys	1511
gat Asp	cat His 385	ctt Leu	aaa Lys	aga Arg	tgg Trp	aac Asn 390	ttt Phe	gtt Val	cat His	gat Asp	ttt Phe 395	gct Ala	gaa Glu	agc Ser	atc Ile	1559
tgt Cys 400	tgg Trp	act Thr	ctt Leu	tta Leu	aat Asn 405	cag Gln	caa Gln	gat Asp	gag Glu	aca Thr 410	gtt Val	gtc Val	tgg Trp	aaa Lys	aag Lys 415	1607
act Thr	atc Ile	aac Asn	acc Thr	aaa Lys 420	tgt Cys	tat Tyr	agt Ser	tcc Ser	cgg Arg 425	aaa Lys	cct Pro	gga Gly	gtg Val	ggc Gly 430	cct Pro	1655
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gaa Glu	ggc Gly 465	agg Arg	aca Thr	aga Arg	tgg Trp	cct Pro 470	agc Ser	cgg Arg	tct Ser	aac Asn	atg Met 475	aac Asn	aag Lys	act Thr	gaa Glu	1799
ctt Leu 480	tca Ser	tta Leu	tat Tyr	ggg Gly	ctt Leu 485	cac His	ccc Pro	gag Glu	gtg Val	ctt Leu 490	gga Gly	gag Glu	gat Asp	gct Ala	gag Glu 495	1847
aac Asn	tgg Trp	aag Lys	ata Ile	aca Thr 500	gtg Val	aga Arg	gaa Glu	tac Tyr	tgg Trp	tct Ser	ctc Leu	ttg Leu	tct Ser	cct Pro 510	ctg Leu	1895
ata Ile	ttc Phe	tct Ser	gat Asp 515	cat His	cca Pro	aaa Lys	aga Arg	ccc Pro 520	ggc Gly	gat Asp	gaa Glu	gat Asp 525	cca Pro	tca Ser	ccg Pro	1943
cct Pro	tat Tyr	aac Asn 530	atg Met	ctc Leu	aga Arg	aac Asn	gta Val 535	ctg Leu	gat Asp	atg Met	aat Asn	gct Ala 540	caa Gln	ttc Phe	ggg Gly	1991
ggg Gly	ctc Leu 545	aat Asn	tcc Ser	gcc Ala	ttg Leu	ttg Leu 550	gaa Glu	gca Ala	aga Arg	aaa Lys	tca Ser 555	gtc Val	tgg Trp	gtc Val	atg Met	2039
aat Asn 560	gtg Val	gtc Val	cct Pro	aca Thr	gct Ala 565	gga Gly	cct Pro	aac Asn	cac His	ctc Leu 570	ccc Pro	atg Met	ata Ile	ctt Leu	gac Asp 575	2087
cgt Arg	ggc Gly	ttt Phe	gtc Val	gga Gly 580	gtt Val	ttg Leu	cac His	aac Asn	tgg Trp 585	tgt Cys	gaa Glu	cca Pro	ttc Phe	ccg Pro 590	act Thr	2135

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Glu 145	Leu	Glu	Tyr	Cys	Asn 150	Ile	Glu	Ser	Glu	Asn 155	Phe	Val	Pro	Cys	Phe 160
Asn	Val	Ser	Glu	Asn 165	Leu	Ala	Leu	Gly	Tyr 170	Ser	Asn	Gly	Asp	Glu 175	Asn
Asp	Arg	Phe	Cys 180	Gly	Pro	Gly	Ser	Lys 185	Gln	Glu	Cys	Leu	Glu 190	Leu	Pro
Pro	Val	Lys 195	Tyr	Arg	Val	Pro	Leu 200	Arg	Trp	Pro	Thr	Gly 205	Lys	Asp	Ile
Ile	Trp 210	His	Ser	Asn	Val	Lys 215	Ile	Thr	Ala	Gln	Glu 220	Val	Val	Ser	Ser
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Phe	Arg	Ser	Ala	Ser 245	Pro	Met	Ser	Asp	Glu 250	Val	Glu	Asp	Tyr	Ser 255	His
Gln	Ile	Ala 260	Glu	Met	Ile	Gly	Ile	Lys 265	Lys	Asp	Asn	Phe	Ile 270	Glu	Ala
Gly	Val	Arg 275	Thr	Ile	Leu	Asp	Ile	Gly 280	Cys	Gly	Tyr	Gly 285	Ser	Phe	Gly
Ala	His 290	Leu	Leu	Ser	Lys	Gln 295	Ile	Leu	Thr	Met	Cys 300	Ile	Ala	Asn	Tyr
Glu 305	Ala	Ser	Gly	Ser	Gln 310	Val	Gln	Leu	Thr	Leu 315	Glu	Arg	Gly	Leu	Pro 320
Ala	Met	Ile	Gly	Ser 325	Phe	Ile	Ser	Lys	Gln 330	Leu	Pro	Tyr	Pro	Ser 335	Leu
Ser	Phe	Asp	Met 340	Leu	His	Cys	Leu	Arg 345	Cys	Gly	Ile	Asp	Trp 350	Asp	Gln
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Gly 370	Tyr	Phe	Val	Trp	Thr	Ser	Pro	Leu	Thr	Asn	Pro	Arg	Asn	Lys	Asp
His 385	Leu	Lys	Arg	Trp	Asn	Phe	Val	His	Asp	Phe	Ala	Glu	Ser	Ile	Cys 400
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Gly 465	Arg	Thr	Arg	Trp	Pro	Ser	Arg	Ser	Asn	Met	Asn	Lys	Thr	Glu	Leu 480
Ser	Leu	Tyr	Gly	Leu	His	Pro	Glu	Val	Leu	Gly	Glu	Asp	Ala	Glu	Asn
Trp	Lys	Ile	Thr	Val	Arg	Glu	Tyr	Trp	Ser	Leu	Leu	Ser	Pro	Leu	Ile
Phe	Ser	Asp	His	Pro	Lys	Arg	Pro	Gly	Asp	Glu	Asp	Pro	Ser	Pro	Pro
Tyr	Asn	Met	Leu	Arg	Asn	Val	Leu	Asp	Met	Asn	Ala	Gln	Phe	Gly	Gly
Leu 545	Asn	Ser	Ala	Leu	Leu	Glu	Ala	Arg	Lys	Ser	Val	Trp	Val	Met	Asn 560
Val	Val	Pro	Thr	Ala	Gly	Pro	Asn	His	Leu	Pro	Met	Ile	Leu	Asp	Arg
Gly	Phe	Val	Gly	Val	Leu	His	Asn	Trp	Cys	Glu	Pro	Phe	Pro	Thr	Tyr
Pro	Arg	Thr	Tyr	Asp	Leu	Val	His	Ala	Asp	Asn	Leu	Leu	Ser	Leu	Gln
Thr	Ser	Gln	Pro	Arg	Lys	Thr	Cys	Leu	Leu	Ile	Asp	Ile	Phe	Thr	Glu
Ile 625	Asp	Arg	Leu	Leu	Arg	Pro	Glu	Gly	Trp	Val	Ile	Ile	Arg	Asp	Thr 640
Ala	Gln	Leu	Val	Glu	Lys	Ala	Arg	Glu	Thr	Ile	Thr	Gln	Leu	Lys	Trp
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Cys	Tyr	Gly	Phe	Phe	Ile	Ala	Ala	Leu	Ile	Val	Asn	Leu	Leu	Arg	Asp	
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Gly Ile Ile Pro Ser Leu Asn Val Ala Ala Gly Leu Leu Gly Phe Phe  
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Ala	Cys	Tyr	Gly	Leu	Ala	Phe	Ser	Gly	Gly	Phe	Gly	Ser	Tyr	Leu	Ile	
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Gln Arg Tyr Leu Pro Ser Asn Glu Pro Asp Pro Glu Ser Tyr Pro Asp  
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Ser	Ser	Ser	Ser	Ser	Lys	Lys	Pro	Leu	Phe	Ala	Asn	Asn	Asn	Thr	Pro					
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Tyr Ala Met Glu Glu Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile	
205 210 215 220	
gaa aaa gat gag att gaa gaa gaa gta gaa gag ata aaa gcc atg agc	842
Glu Lys Asp Glu Ile Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser	
225 230 235	
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Met Asp Ile Phe Asp Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro	
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Phe Glu Leu Ser Phe Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu	
255 260 265	
gag gta atg aag aac gtt gaa agt agt ggt gaa tgt gtt gtt aag gtg	986
Glu Val Met Lys Asn Val Glu Ser Ser Gly Glu Cys Val Val Lys Val	
270 275 280	
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Lys Glu Glu Glu His Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp	
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tcg gtg ata tcc act tgg gga ggt caa ggt cca ccg tgg agt tca gga	1082
Ser Val Ile Ser Thr Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly	
305 310 315	
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Glu Pro Pro Glu Arg Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser	
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Met Val Glu Asn Gly Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly	
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gga tgt tta cca tca agt ggg ttt gga gat gga ggt aga gaa gct aga	1226
Gly Cys Leu Pro Ser Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg	
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Val Ser Arg Tyr Arg Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys	
365 370 375 380	
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Ile Arg Tyr Glu Val Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met	
385 390 395	
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Lys Gly Arg Phe Val Lys Arg Ala Ser Leu Ala Ala Ala Ala Ser Pro	
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Gly	Leu	Met	Ile	Glu	Glu	Glu	Glu	Asp	Asn	Ala	Glu	Ser	Cys	Leu	Asn
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Gly	Phe	Phe	Pro	Thr	Asp	Met	Glu	Leu	Glu	Glu	Phe	Ala	Ala	Asp	Val
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Asp Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro Phe Glu Leu Ser  
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 Phe Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu Glu Val Met Lys  
 260 265 270  
 Asn Val Glu Ser Ser Gly Glu Cys Val Val Lys Val Lys Glu Glu Glu  
 275 280 285  
 His Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp Ser Val Ile Ser  
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 Thr Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly Glu Pro Pro Glu  
 305 310 315 320  
 Arg Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser Met Val Glu Asn  
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 Gly Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly Gly Cys Leu Pro  
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 Ser Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr  
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 Met Asp His Leu Leu Gln His Gln  
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 gat gtt ttt ggg aat tat aac aaa gca aga gaa gca atg gga cta tca 162  
 Asp Val Phe Gly Asn Tyr Asn Lys Ala Arg Glu Ala Met Gly Leu Ser  
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tat Tyr 25	tca Ser	tca Ser	aac Asn	cca Pro	aca Thr 30	ccg Pro	tta Leu	gat Asp	aac Asn	gac Asp 35	cag Gln	aag Lys	aaa Lys	cct Pro	tct Ser 40	210
cct Pro	gca Ala	acg Thr	gct Ala	gtg Val 45	aca Thr	agg Arg	cca Pro	cag Gln	cct Pro 50	ccg Pro	gag Glu	cta Leu	gct Ala	ctc Leu 55	agg Arg	258
tgt Cys	cca Pro	cgt Arg	tgc Cys 60	gac Asp	tca Ser	aca Thr	aac Asn	aca Thr 65	aag Lys	ttt Phe	tgt Cys	tac Tyr	tac Tyr 70	aac Asn	aac Asn	306
tac Tyr	agt Ser	ctc Leu 75	act Thr	cag Gln	cct Pro	cgc Arg	tac Tyr 80	ttc Phe	tgc Cys	aaa Lys	tca Ser	tgc Cys 85	cgg Arg	aga Arg	tat Tyr	354
tgg Trp	act Thr 90	aaa Lys	ggg Gly	gga Gly	act Thr	cta Leu 95	agg Arg	aac Asn	atc Ile	ccc Pro	gtg Val 100	ggg Gly	gga Gly	ggc Gly	tgc Cys	402
cgg Arg 105	aaa Lys	aac Asn	aaa Lys	cga Arg	tcc Ser 110	aca Thr	tct Ser	tcg Ser	gct Ala	gca Ala 115	aga Arg	agc Ser	ctc Leu	aga Arg	acc Thr 120	450
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ttt Phe	aat Asn	ggg Gly	tat Tyr 140	agt Ser	aac Asn	aat Asn	gaa Glu	cat His 145	att Ile	gat Asp	ctg Leu	agc Ser	tta Leu 150	gcc Ala	ttt Phe	546
gcc Ala	ttg Leu 155	ctg Leu	aac Asn	aaa Lys	caa Gln	cat His	ccg Pro 160	ggg Gly	agt Ser	tct Ser	tca Ser	cag Gln 165	cta Leu	ggg Gly	ttt Phe	594
cat His 170	tca Ser	gaa Glu	ctc Leu	ggg Gly	agc Ser	tct Ser 175	cat His	cag Gln	tct Ser	gac Asp	atg Met 180	gaa Glu	ggg Gly	atg Met	ttt Phe	642
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cag Gln	atg Met	aat Asn	gga Gly 220	gag Glu	agc Ser	ttt Phe	gga Gly	atg Met 225	atg Met	aac Asn	ata Ile	gga Gly	gga Gly 230	ggg Gly	ggg Gly	786
ggg Gly	cat His 235	gta Val	gat Asp	cag Gln	att Ile	gat Asp 240	tca Ser	ggg Gly	aga Arg	gag Glu	atg Met 245	tgg Trp	acc Thr	aat Asn	atg Met	834

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Phe	Cys	Lys	Ser	Cys	Arg	Arg	Tyr	Trp	Thr	Lys	Gly	Gly	Thr	Leu	Arg	
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Asn	Ile	Pro	Val	Gly	Gly	Gly	Cys	Arg	Lys	Asn	Lys	Arg	Ser	Thr	Ser	
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Gln Ser Asp Met Glu Gly Met Phe Gly Thr Ser Gln Gln Lys Glu Asn  
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Ala Thr Tyr Ala Phe Gly Asn Gly Ser Ser Gly Leu Gly Asp Pro Ser  
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Arg Val Leu Trp Gly Phe Pro Trp Gln Met Asn Gly Glu Ser Phe Gly  
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cct aac tct tca tta tca aac aat ctc cag aga ctc cca tgg aac caa 146  
Pro Asn Ser Ser Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln  
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aca ttc gat cct aca tca gat ctt cgc aag ata gac gtg aac agt ttt 194  
Thr Phe Asp Pro Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe  
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Pro Ser Thr Val Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn  
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Ile Ser Gly Thr Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr  
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0034519 001240

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 175 180

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Thr	Ser	Thr	Asp	Glu	Gln	Ser	Pro	Arg	Gly	Tyr	Gly	Ser	Asn	Tyr	Gln	
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Ser	Met	Leu	Glu	Gly	Tyr	Asp	Glu	Asp	Ala	Thr	Leu	Ile	Glu	Glu	Tyr	
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Ser	Gly	Asn	His	His	His	Met	Gly	Leu	Ser	Glu	Lys	Lys	Arg	Arg	Leu	
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aaa	gtt	gac	caa	gtc	aaa	gct	ctt	gag	aag	aat	ttc	gaa	ctt	gag	aat	239
Lys	Val	Asp	Gln	Val	Lys	Ala	Leu	Glu	Lys	Asn	Phe	Glu	Leu	Glu	Asn	
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caa cct cgt caa gta gct gtt tgg ttt cag aac cgt cgt gca cgg tgg 335  
 Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp  
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aaa aca aaa cag ctt gaa aaa gat tac ggt gtt ctt aag ggt caa tac 383  
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 130 135 140

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 145 150 155

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gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca ctt cat tgg tac 863  
 Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr  
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 Ser Ala Ser Asp His Trp Thr  
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Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser Ser Asp Ser Cys Asp  
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 Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser Asp Asn Gly Arg Leu  
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 Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu Ser Gly Glu Glu Ala  
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 Met Met Met Gly Lys  
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 Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln Asn His Asn  
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 Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser Asp Leu Arg  
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1221

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Tyr	Leu	Lys	Arg	Cys	Val	Glu	Lys	Leu	Thr	Glu	Glu	Asn	Arg	Arg	Leu
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Gln	Lys	Glu	Ala	Met	Glu	Leu	Arg	Thr	Leu	Lys	Leu	Ser	Pro	Gln	Phe
			210			215					220				
Tyr	Gly	Gln	Met	Thr	Pro	Pro	Thr	Thr	Leu	Ile	Met	Cys	Pro	Ser	Cys
			225		230					235					240

66160-6754660

Glu Arg Val Ala Gly Pro Ser Ser Ser Asn His His His Asn His Arg  
245 250 255

Pro Val Ser Ile Asn Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His  
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Met Gln Thr Glu Glu Leu Leu Ser Pro Pro Gln Thr  
1 5 10

cct tgg tgg aat gct ttt gga tct cag ccg ttg act aca gag agc ctt 159  
Pro Trp Trp Asn Ala Phe Gly Ser Gln Pro Leu Thr Thr Glu Ser Leu  
15 20 25

tcc ggc gaa gct tct gat tca ttc acc gga gtt aag gca gtt act acg 207  
Ser Gly Glu Ala Ser Asp Ser Phe Thr Gly Val Lys Ala Val Thr Thr  
30 35 40

gag gca gaa caa ggt gtg gtg gat aaa caa act tct aca act ctc ttc 255  
Glu Ala Glu Gln Gly Val Val Asp Lys Gln Thr Ser Thr Thr Leu Phe  
45 50 55 60

act ttc tca cct ggt ggt gaa aag agt tca aga gat gtg cca aag cct 303  
Thr Phe Ser Pro Gly Gly Glu Lys Ser Ser Arg Asp Val Pro Lys Pro  
65 70 75

cat gtt gct ttc gcg atg caa tca gct tgc ttc gag ttt gga ttt gct 351  
His Val Ala Phe Ala Met Gln Ser Ala Cys Phe Glu Phe Gly Phe Ala  
80 85 90

cag cca atg atg tac aca aag cat cct cat gtt gaa caa tac tat gga 399  
Gln Pro Met Met Tyr Thr Lys His Pro His Val Glu Gln Tyr Tyr Gly  
95 100 105

gtt gtt tca gca tac gga tct cag agg tct tcg ggc cga gta atg att 447  
Val Val Ser Ala Tyr Gly Ser Gln Arg Ser Ser Gly Arg Val Met Ile  
110 115 120

cca ctg aag atg gag aca gaa gaa gat ggt acc atc tat gtg aac tca 495  
Pro Leu Lys Met Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser  
125 130 135 140

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gaa aaa ctg agt aga tgc cgt aag cca tat atg cat cac tca cgc cat 591  
Glu Lys Leu Ser Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His  
160 165 170  
  
ctc cat gct atg cgc cgt cct aga gga tct ggc ggg cgt ttc ttg aac 639  
Leu His Ala Met Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn  
175 180 185  
  
acc aag aca gct gat gcg gct aag cag tct aag ccg agt aat tct cag 687  
Thr Lys Thr Ala Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln  
190 195 200  
  
agt tct gaa gtc ttt cat ccg gaa aat gag acc ata aac tca tcg agg 735  
Ser Ser Glu Val Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg  
205 210 215 220  
  
gaa gca aat gag tca aat ctc tcg gat tct gca gtt aca agt atg gat 783  
Glu Ala Asn Glu Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp  
225 230 235  
  
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Tyr Phe Leu Ser Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro  
240 245 250  
  
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Ile Lys Trp Asn Ala Ala Ala Met Asp Ile Gly Cys Cys Lys Leu Asn  
255 260 265  
  
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Ile  
  
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aagatctctg aactagtga taacatttcc tagcatcatg tttcaactag tgtgtgttgt 1172  
  
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<400> 130

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 210 215 220

gag aag aaa cgt agc tgt cgc cga cct ctc tca gat cac aat gca aga 780  
 Glu Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg  
 225 230 235

cgt cgc aag cca aat cct gga agg aca tat gat ggg aaa cca cag gtg 828  
 Arg Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Gln Val  
 240 245 250 255

gat ttt gta tgg aac aga ttt gca ctt atc cat cca aga agt gag gaa 876  
 Asp Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu  
 260 265 270

aag ttt cta tgg ccc agt tca aag cct gta cca tca aga gtc tta atg 924  
 Lys Phe Leu Trp Pro Ser Ser Lys Pro Val Pro Ser Arg Val Leu Met  
 275 280 285

ccg cag cct gca aag acc gag att tcc aat aag ctg ttc acc gag cac 972  
 Pro Gln Pro Ala Lys Thr Glu Ile Ser Asn Lys Leu Phe Thr Glu His  
 290 295 300

agt aga ttt gga ttg ttg gac ccc aaa aca aaa tcc gca aga gcg gag 1020  
 Ser Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu  
 305 310 315

tta ttc agt aaa gaa aag gtc aca atc tct tca cac atg ggt gct tct 1068  
 Leu Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser  
 320 325 330 335

caa gat ctt gat ggt gct ctc tct ctt ctg tca aat tca aca aca tgg 1116  
 Gln Asp Leu Asp Gly Ala Leu Ser Leu Leu Ser Asn Ser Thr Thr Trp  
 340 345 350

gtt tct tcc tct gac caa cca aga cgt ttt acc ctt gat cac cat ccc 1164  
 Val Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro  
 355 360 365

tca agc aac ctc caa ccc gta gct aac cgg tct gcg gct caa ctc agt 1212  
 Ser Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser  
 370 375 380

tca gtg tcc ggc tat tgg cag ccg gac cca ccc gca gtt gaa ggc ccg 1260  
 Ser Val Ser Gly Tyr Trp Gln Pro Asp Pro Pro Ala Val Glu Gly Pro  
 385 390 395

acc gct ctg cat aga aat ggg gca ggc cag ttt aat gaa aac tac ttc 1308  
 Thr Ala Leu His Arg Asn Gly Ala Gly Gln Phe Asn Glu Asn Tyr Phe  
 400 405 410 415

agc ttg aac cag ttt tat aac tgaaagctgt atgccttta atcctattta 1359  
 Ser Leu Asn Gln Phe Tyr Asn  
 420

ggatcaagca agctagtgat aagttaagat aggagctgtg aaacttgcaa gacaccaa 1419

cctctcttat ttctttgtcc aaatattttc atggggttaga gagctttgac aattgtcttt 1479  
 aatatcaact ttatcgtgtt atacattagg attataaaaa aaaaaaaaaa a 1530

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 Met Glu Trp Glu Ile Asp Gly Phe Asp Cys Thr Ser Leu Tyr Ser Ser  
 35 40 45  
 Ser Phe Ala Tyr Ala Gly Ser Ser Gly Ser Asp Ile Ala His Ala Phe  
 50 55 60  
 Ser Lys Ser Ser Lys Ser Thr Ser Ile Ser Ser Ser Ser Ala Glu Val  
 65 70 75 80  
 Arg Thr His Asn Phe Thr Ser Glu Thr Gly Glu Ser Leu Pro Gly Glu  
 85 90 95  
 Phe Ala Lys Gly Ile Asp Thr Ser Pro Thr Leu Glu Leu Ser Phe Gly  
 100 105 110  
 Ser Gly Asp Pro Val Leu Gly Leu Lys Leu Ala Lys Arg Thr Tyr Phe  
 115 120 125  
 Glu Asp Phe Trp Glu Val Glu Asn Ala Lys Gly Leu Gly Leu Pro Val  
 130 135 140  
 Thr Leu Ala Ser Ser Ser Val Ser Pro Val Lys Lys Ser Lys Ser Ile  
 145 150 155 160  
 Pro Gln Thr Leu Gln Thr Pro His Cys Gln Val Glu Gly Cys Asn Leu  
 165 170 175  
 Asp Leu Ser Ser Ala Lys Asp Tyr His Arg Lys His Arg Ile Cys Glu  
 180 185 190  
 Asn His Ser Lys Phe Pro Lys Val Val Val Ser Gly Val Glu Arg Arg  
 195 200 205  
 Phe Cys Gln Gln Cys Ser Arg Phe His Cys Leu Ser Glu Phe Asp Glu  
 210 215 220

03446154660







Met Arg Lys Glu Arg Thr Thr Asp Leu Asn Leu Leu Pro Ser Ser Pro  
210 215 220

Ser Ser Asp His Ala Ser Ser Gly Val Thr Thr Glu Ile Phe Ser Ser  
225 230 235 240

Ser Asp Glu Glu Thr Ser Ser Cys Asn Ser Phe Arg  
245 250

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<223> G462

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acg gag ctg aga ttg ggg ctt ccg ggg aga gat gtg gca gag aag atg 99  
Thr Glu Leu Arg Leu Gly Leu Pro Gly Arg Asp Val Ala Glu Lys Met 25  
15 20

atg aag aag aga gct ttc acg gag atg aat atg acg tcg tcg ggt agt 147  
Met Lys Lys Arg Ala Phe Thr Glu Met Asn Met Thr Ser Ser Gly Ser 40  
30 35

aat agt gat caa tgt gaa agc ggc gtc gtt tca tct ggt ggt gac gct 195  
Asn Ser Asp Gln Cys Glu Ser Gly Val Val Ser Ser Gly Gly Asp Ala 55  
45 50

gag aag gtt aat gat tcg ccg gcg gcg aaa agc cag gtg gtg ggg tgg 243  
Glu Lys Val Asn Asp Ser Pro Ala Ala Lys Ser Gln Val Val Gly Trp 70  
60 65

cca ccg gtt tgt tct tac cgg aag aaa aac agc tgt aag gaa gct tcg 291  
Pro Pro Val Cys Ser Tyr Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser 90  
75 80 85

acc acg aaa gtg ggg tta ggg tat gtg aaa gtg agc atg gat ggt gtg 339  
Thr Thr Lys Val Gly Leu Gly Tyr Val Lys Val Ser Met Asp Gly Val 105  
95 100

cct tat ttg agg aag atg gat ctt ggt tcg agc caa ggc tat gat gat 387  
Pro Tyr Leu Arg Lys Met Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp 120  
110 115

cta gcc ttt gct ctt gat aag ctc ttc ggt ttc cgt ggc atc ggt gtg 435  
Leu Ala Phe Ala Leu Asp Lys Leu Phe Gly Phe Arg Gly Ile Gly Val 135  
125 130

000441-6754660

gcc ttg aaa gat ggt gac aac tgc gaa tac gtt acc ata tac gaa gac 483  
 Ala Leu Lys Asp Gly Asp Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp  
 140 145 150

aaa gat gga gac tgg atg ctc gcc ggt gat gta cct tgg ggg atg ttt 531  
 Lys Asp Gly Asp Trp Met Leu Ala Gly Asp Val Pro Trp Gly Met Phe  
 155 160 165 170

cta gag tca tgc aag agg ttg aga ata atg aaa aga tcg gat gct acc 579  
 Leu Glu Ser Cys Lys Arg Leu Arg Ile Met Lys Arg Ser Asp Ala Thr  
 175 180 185

ggg ttt ggg ctg cag cct aga gga gta gac gag tgatgatgac ttgaacaaga 632  
 Gly Phe Gly Leu Gln Pro Arg Gly Val Asp Glu  
 190 195

agcaaggagc tgggttcatta atttaattctt aaacttgatc atcaagatcc tttagaacat 692

ttttcctatt catgttatat aaatatatat gttatagtat attattttgc aacaaaaattt 752

catgttaaaa aaaaaaaaaa aaaaaaa 779

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<211> 197

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<213> Arabidopsis thaliana

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<223> G462

<400> 136

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Leu Pro Gly Arg Asp Val Ala Glu Lys Met Met Lys Lys Arg Ala Phe  
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Thr Glu Met Asn Met Thr Ser Ser Gly Ser Asn Ser Asp Gln Cys Glu  
 35 40 45

Ser Gly Val Val Ser Ser Gly Gly Asp Ala Glu Lys Val Asn Asp Ser  
 50 55 60

Pro Ala Ala Lys Ser Gln Val Val Gly Trp Pro Pro Val Cys Ser Tyr  
 65 70 75 80

Arg Lys Lys Asn Ser Cys Lys Glu Ala Ser Thr Thr Lys Val Gly Leu  
 85 90 95

Gly Tyr Val Lys Val Ser Met Asp Gly Val Pro Tyr Leu Arg Lys Met  
 100 105 110

Asp Leu Gly Ser Ser Gln Gly Tyr Asp Asp Leu Ala Phe Ala Leu Asp  
 115 120 125

Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp  
 130 135 140

Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met  
145 150 155 160

Leu Ala Gly Asp Val Pro Trp Gly Met Phe Leu Glu Ser Cys Lys Arg  
165 170 175

Leu Arg Ile Met Lys Arg Ser Asp Ala Thr Gly Phe Gly Leu Gln Pro  
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Arg Gly Val Asp Glu  
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tcaatttgat cgtcctgaat tcatcgtcct atttaggggt tcatcacaa tctgaagagg 180

aggtc atg gac gtt tct gct aga aag tca caa aaa gct ggg cgc gaa aag 230

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys  
1 5 10 15

ttg agg agg gaa aaa ctg aat gag cat ttt gtt gaa ctg gga aat gta 278

Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val  
20 25 30

ctc gat cca gag aga ccc aag aat gac aaa gcc acg att ctg act gat 326

Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp  
35 40 45

act gtt cag ttg ttg aaa gag ctc aca tct gaa gtc aac aaa ctg aaa 374

Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys  
50 55 60

tct gag tac acc gca ttg aca gat gag tcc cgc gag ttg aca cag gag 422

Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu  
65 70 75

aaa aac gac ctg aga gaa gaa aag aca tcg ctg aaa tca gat ata gag 470

Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu  
80 85 90 95

aat ctc aat ctt caa tac cag cag aga tta agg tca atg tct cca tgg 518

Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp  
100 105 110

CGAGAGGCTA GAGAATCGAG AATCGATCTT CGCCGAACCA CCTTGCTCTT TCTTAGCTCA 60





&lt;220&gt;

&lt;223&gt; G782

&lt;400&gt; 138

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Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val Leu
          20              25              30

Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp Thr
          35              40              45

Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
 50              55              60

Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
 65              70              75              80

Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
          85              90              95

Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
          100              105              110

Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro
 115              120              125

Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
 130              135              140

Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
 145              150              155              160

Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
          165              170              175

Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
 180              185              190

Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
 195              200              205

Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
 210              215              220

Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
 225              230              235              240

Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser
          245              250              255

Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser Ser
          260              265              270

Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
 275              280

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090416154660



tct gct aca act ctt cat cct cct gca aca gtt ctt gtc ctt cca ata 641  
 Ser Ala Thr Thr Leu His Pro Pro Ala Thr Val Leu Val Leu Pro Ile  
                   175                                  180                                  185

caa cct gat ccc cag aca caa gat atc tca gaa atg act caa gcg cag 689  
 Gln Pro Asp Pro Gln Thr Gln Asp Ile Ser Glu Met Thr Gln Ala Gln  
                   190                                  195                                  200

cag cct ttg atg ttt aat agc tca aat gtg agt aac cca tgt cca agg 737  
 Gln Pro Leu Met Phe Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg  
                   205                                  210                                  215

tat gct agc gcg gct gac tcg tgg tct tct cgg cta ctt gga gag cgg 785  
 Tyr Ala Ser Ala Ala Asp Ser Trp Ser Ser Arg Leu Leu Gly Glu Arg  
                   220                                  225                                  230                                  235

ctg aaa gcc agt gaa tgaggtcttg aacggctcca catggagtag caacgcaagt 840  
 Leu Lys Ala Ser Glu  
                                   240

tataagacat ggcaacttat gaaggactct ggttttgtat tttttaatac atcgttctga 900

tgtccttggtg ggtttggcct tggctatttc ttgtttttga tggttgttca taggatcagg 960

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aaaaaaaaa 1027

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Ala Asp Glu Arg Cys Arg Lys Gly Lys Val Pro Lys Arg Ile Asn Lys  
                   20                                  25                                  30

Ala Val Arg Glu Arg Leu Lys Arg Glu His Leu Asn Glu Leu Phe Ile  
                   35                                  40                                  45

Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln Asn Ser Gly Lys Ala  
           50                                  55                                  60

Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys Asp Val Phe Gly Gln  
           65                                  70                                  75                                  80

Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu Leu Ser Glu Ser Ser  
                   85                                  90                                  95

0034510 09139





gaa gct cag aaa ctt ggc gtt gga cat ttc tca aac caa tct 1185  
 Glu Ala Gln Lys Leu Gly Val Gly His Phe Ser Asn Gln Ser  
           240                          245                          250

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 ggcaggatgg tatctatttt atgtttgaat ctctctatgt attttgcttt ttgtgtgtta 1365  
 ctgcttcgat gaagaagcaa ggtttgaaca agtacttggtg gatttgattt gagattttaa 1425  
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                           20                          25                          30  
 Pro Pro Cys Ala Lys Leu Pro Tyr His Gly Val Glu Leu Gln Pro Ser  
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 Ala Val Cys Pro Lys Asn Phe Val Ile Phe Asp Gln Thr Tyr Asp Arg  
                           50                          55                          60  
 Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu Met Asn Thr  
   65                          70                          75                          80  
 Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu Tyr Val Gly  
                           85                          90                          95  
 Gly Ser Tyr Gly Asn Tyr Gly Asn Tyr Glu Gln Glu Val Ser Ser Ser  
                           100                          105                          110  
 Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser Ala Asp Glu  
                           115                          120                          125  
 Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp Gly Gly Asp  
                           130                          135                          140  
 Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp Tyr Gly Asn  
   145                          150                          155                          160  
 Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn Asn Asn Asn  
                           165                          170                          175

Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala Ser Ser Ser  
 180 185 190

Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met Met Gly Val  
 195 200 205

Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr Ala Cys Val  
 210 215 220

Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile Glu Ala Gln  
 225 230 235 240

Lys Leu Gly Val Gly His Phe Ser Asn Gln Ser  
 245 250

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 <223> G793

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ctttactcgt ttccttc atg gct aat aac aac aac atc cca cat gat agc 170  
 Met Ala Asn Asn Asn Asn Ile Pro His Asp Ser  
 1 5 10

atc tcc gat cca tct cct acc gac gat ttc ttc gag cag atc ctc ggg 218  
 Ile Ser Asp Pro Ser Pro Thr Asp Asp Phe Phe Glu Gln Ile Leu Gly  
 15 20 25

ctt tcc aac ttc tcc ggt tct tca ggt tot ggt ctc tct gga atc ggc 266  
 Leu Ser Asn Phe Ser Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly  
 30 35 40

ggc gtg ggt cca cct ccg atg atg ctt cag ctt ggt tca ggc aac gaa 314  
 Gly Val Gly Pro Pro Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu  
 45 50 55

ggg aat cat aat cat atg ggt gcc att gga gga ggt gga cct gta ggg 362  
 Gly Asn His Asn His Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly  
 60 65 70 75

ttt cat aat cag atg ttt ccg ttg gga tta agt ctc gat caa ggg aaa 410  
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Lys Arg Lys Ser Trp Gly Gln Gln Leu Pro Glu Pro Lys Thr Asn Leu																
75 80 85																
cct ccg agg aag cgc gca aag act caa gat gaa aaa gag caa cgg cgt																522
Pro Pro Arg Lys Arg Ala Lys Thr Gln Asp Glu Lys Glu Gln Arg Arg																
90 95 100																
gtt gag cgc gtc cta cgc aat cgt aga gcg gcc caa tca tca cga gaa																570
Val Glu Arg Val Leu Arg Asn Arg Arg Ala Ala Gln Ser Ser Arg Glu																
105 110 115																



















aaaagatttc gggtcg atg aac atg gat gaa ctc ctg aag agc ata tgg act 52  
 Met Asn Met Asp Glu Leu Leu Lys Ser Ile Trp Thr  
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 Ala Glu Glu Ala Gln Ala Met Ala Met Thr Ser Ala Pro Ala Ala Thr  
 15 20 25

gcg gta gcg caa cct ggt gct ggt atc cca ccc cca ggt ggg aat ctc 148  
 Ala Val Ala Gln Pro Gly Ala Gly Ile Pro Pro Pro Gly Gly Asn Leu  
 30 35 40

cag agg caa ggt tcg ttg acg ttg cct aga aca att agt cag aag act 196  
 Gln Arg Gln Gly Ser Leu Thr Leu Pro Arg Thr Ile Ser Gln Lys Thr  
 45 50 55 60

gtt gat gag gtg tgg aaa tgt ttg atc acc aag gat ggt aat atg gaa 244  
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 Gly Ser Ser Gly Gly Gly Gly Glu Ser Asn Val Pro Pro Gly Arg Gln  
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cag act tta ggg gaa atg aca ctt gaa gaa ttt ctg ttc cgt gct ggg 340  
 Gln Thr Leu Gly Glu Met Thr Leu Glu Glu Phe Leu Phe Arg Ala Gly  
 95 100 105

gtt gta aga gaa gat aac tgt gtt caa cag atg ggt cag gtc aac gga 388  
 Val Val Arg Glu Asp Asn Cys Val Gln Gln Met Gly Gln Val Asn Gly  
 110 115 120

aac aat aac aat ggg ttt tat ggt aac agc act gct gct ggc ggc tta 436  
 Asn Asn Asn Asn Gly Phe Tyr Gly Asn Ser Thr Ala Ala Gly Gly Leu  
 125 130 135 140

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 Gly Phe Gly Phe Gly Gln Pro Asn Gln Asn Ser Ile Thr Phe Asn Gly  
 145 150 155

act aat gat tct atg atc ttg aat cag cca cct ggt tta ggg ctc aaa 532  
 Thr Asn Asp Ser Met Ile Leu Asn Gln Pro Pro Gly Leu Gly Leu Lys  
 160 165 170

atg ggt gga aca atg cag cag caa caa caa caa cag cag ttg ctt cag 580  
 Met Gly Gly Thr Met Gln Gln Gln Gln Gln Gln Gln Leu Leu Gln  
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cag caa caa cag cag atg cag cag ctg aat cag cct cat cca cag cag 628  
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 190 195 200

cgg ctg cct caa acc att ttt cct aaa caa gca aac gta gca ttt tct 676  
 Arg Leu Pro Gln Thr Ile Phe Pro Lys Gln Ala Asn Val Ala Phe Ser  
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66E160-61516660

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225 230 235

tct atc aac aat aat aat gga tta gct agt tac gga gga acc ggg gtc 772  
Ser Ile Asn Asn Asn Asn Gly Leu Ala Ser Tyr Gly Gly Thr Gly Val  
240 245 250

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Thr Val Ala Ala Thr Ser Pro Gly Thr Ser Ser Ala Glu Asn Asn Ser  
255 260 265

tta tca cca gtt ccg tat gtg ctt aat cga gga cga aga agc aat aca 868  
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270 275 280

ggt cta gag aag gtt atc gag agg agg caa agg aga atg atc aag aat 916  
Gly Leu Glu Lys Val Ile Glu Arg Arg Gln Arg Arg Met Ile Lys Asn  
285 290 295 300

cgg gaa tca gct gct aga tca aga gct cga aag cag gct tat aca ttg 964  
Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Leu  
305 310 315

gaa ctg gaa gcc gaa att gaa aag ctc aag aaa acg aat caa gaa ctg 1012  
Glu Leu Glu Ala Glu Ile Glu Lys Leu Lys Lys Thr Asn Gln Glu Leu  
320 325 330

cag aaa aaa cag gct gaa atg gtg gaa atg cag aag aat gag ctg aaa 1060  
Gln Lys Lys Gln Ala Glu Met Val Glu Met Gln Lys Asn Glu Leu Lys  
335 340 345

gaa acg tcg aag cga ccg tgg ggc agc aaa agg caa tgc ttg aga agg 1108  
Glu Thr Ser Lys Arg Pro Trp Gly Ser Lys Arg Gln Cys Leu Arg Arg  
350 355 360

aca tta acc gga cca tgg tgaaggatga agcaacaaga acggatgaac 1156  
Thr Leu Thr Gly Pro Trp  
365 370

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aaattgagtg aaagatctag gttacagagt aggagagagt tttcattatg aataaatgac 1276

attttgtgcc ctgacctttg ttagtttagg tttagattat cctctgttat tgacttattg 1336

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&lt;211&gt; 370

&lt;212&gt; PRT

&lt;213&gt; Arabidopsis thaliana

&lt;220&gt;

&lt;223&gt; G1058

&lt;400&gt; 164

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Gln	Ala	Met	Ala	Met	Thr	Ser	Ala	Pro	Ala	Ala	Thr	Ala	Val	Ala	Gln	20	25	30	
Pro	Gly	Ala	Gly	Ile	Pro	Pro	Pro	Gly	Gly	Asn	Leu	Gln	Arg	Gln	Gly	35	40	45	
Ser	Leu	Thr	Leu	Pro	Arg	Thr	Ile	Ser	Gln	Lys	Thr	Val	Asp	Glu	Val	50	55	60	
Trp	Lys	Cys	Leu	Ile	Thr	Lys	Asp	Gly	Asn	Met	Glu	Gly	Ser	Ser	Gly	65	70	75	80
Gly	Gly	Gly	Glu	Ser	Asn	Val	Pro	Pro	Gly	Arg	Gln	Gln	Thr	Leu	Gly	85	90	95	
Glu	Met	Thr	Leu	Glu	Glu	Phe	Leu	Phe	Arg	Ala	Gly	Val	Val	Arg	Glu	100	105	110	
Asp	Asn	Cys	Val	Gln	Gln	Met	Gly	Gln	Val	Asn	Gly	Asn	Asn	Asn	Asn	115	120	125	
Gly	Phe	Tyr	Gly	Asn	Ser	Thr	Ala	Ala	Gly	Gly	Leu	Gly	Phe	Gly	Phe	130	135	140	
Gly	Gln	Pro	Asn	Gln	Asn	Ser	Ile	Thr	Phe	Asn	Gly	Thr	Asn	Asp	Ser	145	150	155	160
Met	Ile	Leu	Asn	Gln	Pro	Pro	Gly	Leu	Gly	Leu	Lys	Met	Gly	Gly	Thr	165	170	175	
Met	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Leu	Leu	Gln	Gln	Gln	Gln	Gln	180	185	190	
Gln	Met	Gln	Gln	Leu	Asn	Gln	Pro	His	Pro	Gln	Gln	Arg	Leu	Pro	Gln	195	200	205	
Thr	Ile	Phe	Pro	Lys	Gln	Ala	Asn	Val	Ala	Phe	Ser	Ala	Pro	Val	Asn	210	215	220	
Ile	Thr	Asn	Lys	Gly	Phe	Ala	Gly	Ala	Ala	Asn	Asn	Ser	Ile	Asn	Asn	225	230	235	240
Asn	Asn	Gly	Leu	Ala	Ser	Tyr	Gly	Gly	Thr	Gly	Val	Thr	Val	Ala	Ala	245	250	255	
Thr	Ser	Pro	Gly	Thr	Ser	Ser	Ala	Glu	Asn	Asn	Ser	Leu	Ser	Pro	Val	260	265	270	
Pro	Tyr	Val	Leu	Asn	Arg	Gly	Arg	Arg	Ser	Asn	Thr	Gly	Leu	Glu	Lys	275	280	285	
Val	Ile	Glu	Arg	Arg	Gln	Arg	Arg	Met	Ile	Lys	Asn	Arg	Glu	Ser	Ala	290	295	300	

66160 6151660

Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Leu Glu Leu Glu Ala  
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Glu Ile Glu Lys Leu Lys Lys Thr Asn Gln Glu Leu Gln Lys Lys Gln  
 325 330 335

Ala Glu Met Val Glu Met Gln Lys Asn Glu Leu Lys Glu Thr Ser Lys  
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Pro Trp  
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 acaaatcggg tatgggggaa tttgggtttt aagatagcgt gatctgtaat aataagtggg 180  
 tcgcgatcgt gatcaagaaa ctggtggctg atagtgatat gcatatttga gag atg 236  
 Met  
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 gtg ttc aag aga aag tta gat tgc ctt tcc gtg gga ttt gat ttt ccc 284  
 Val Phe Lys Arg Lys Leu Asp Cys Leu Ser Val Gly Phe Asp Phe Pro  
 5 10 15  
 aac att ccc aga gct cct cgt tca tgc agg agg aag gtt cta aac aag 332  
 Asn Ile Pro Arg Ala Pro Arg Ser Cys Arg Arg Lys Val Leu Asn Lys  
 20 25 30  
 agg att gat cat gat gat gat aac act cag atc tgt gca att gac tta 380  
 Arg Ile Asp His Asp Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp Leu  
 35 40 45  
 cta gct ttg gct gga aag att cta cag gaa agc gag agt tcc tct gcg 428  
 Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser Ala  
 50 55 60 65  
 tct tct aat gca ttt gaa gaa att aag caa gag aaa gta gaa aat tgc 476  
 Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys  
 70 75 80

655160" 51546660



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Lys	Thr	Ile	Lys	Ser	Glu	Ser	Ser	Asp	Gln	Gly	Asn	Ser	Val	Ser	Lys	
			85					90					95			
cct	act	tat	gat	atc	tct	act	gag	aag	tgt	gtg	gtg	aac	agt	tgt	ttt	572
Pro	Thr	Tyr	Asp	Ile	Ser	Thr	Glu	Lys	Cys	Val	Val	Asn	Ser	Cys	Phe	
		100					105					110				
tca	ttt	ccg	gat	agt	gac	ggc	gtt	ttg	gag	cgg	act	ccg	atg	tct	gat	620
Ser	Phe	Pro	Asp	Ser	Asp	Gly	Val	Leu	Glu	Arg	Thr	Pro	Met	Ser	Asp	
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tac	aag	aag	att	cat	ggc	ttg	atg	gat	gta	ggg	tgt	gaa	aac	aag	aat	668
Tyr	Lys	Lys	Ile	His	Gly	Leu	Met	Asp	Val	Gly	Cys	Glu	Asn	Lys	Asn	
130					135					140					145	
gta	aat	aat	ggg	ttc	gag	caa	gga	gaa	gca	acc	gat	cgc	gtg	ggc	gat	716
Val	Asn	Asn	Gly	Phe	Glu	Gln	Gly	Glu	Ala	Thr	Asp	Arg	Val	Gly	Asp	
				150				155						160		
gga	ggc	tta	gtc	act	gat	act	tgc	aac	tta	gag	gat	gca	act	gcg	tta	764
Gly	Gly	Leu	Val	Thr	Asp	Thr	Cys	Asn	Leu	Glu	Asp	Ala	Thr	Ala	Leu	
		165					170					175				
ggc	ctg	cag	ttt	ccg	aaa	tca	gtc	tgt	gtg	ggc	ggc	gat	tta	aaa	tca	812
Gly	Leu	Gln	Phe	Pro	Lys	Ser	Val	Cys	Val	Gly	Gly	Asp	Leu	Lys	Ser	
	180						185					190				
cca	tcc	acc	ttg	gat	atg	acc	cct	aat	ggc	tcc	tat	gct	aga	cat	ggg	860
Pro	Ser	Thr	Leu	Asp	Met	Thr	Pro	Asn	Gly	Ser	Tyr	Ala	Arg	His	Gly	
	195					200					205					
aac	cat	act	aac	cta	ggc	aga	aaa	gat	gat	gat	gaa	aaa	ttc	tat	agt	908
Asn	His	Thr	Asn	Leu	Gly	Arg	Lys	Asp	Asp	Asp	Glu	Lys	Phe	Tyr	Ser	
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tac	cat	aaa	ctt	agc	aat	aaa	ttt	aag	tcg	tat	agg	tgt	cca	aca	att	956
Tyr	His	Lys	Leu	Ser	Asn	Lys	Phe	Lys	Ser	Tyr	Arg	Cys	Pro	Thr	Ile	
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cga	aga	ata	aga	aag	tcc	atg	tcg	tcc	aaa	tac	tgg	aaa	caa	gtt	cca	1004
Arg	Arg	Ile	Arg	Lys	Ser	Met	Ser	Ser	Lys	Tyr	Trp	Lys	Gln	Val	Pro	
			245					250					255			
aaa	gat	ttt	gga	tac	agt	aga	gct	gat	gtg	ggc	gtg	aag	act	ctt	tat	1052
Lys	Asp	Phe	Gly	Tyr	Ser	Arg	Ala	Asp	Val	Gly	Val	Lys	Thr	Leu	Tyr	
	260						265					270				
cgc	aaa	aga	aaa	tca	tgt	tat	ggc	tac	aac	gca	tgg	cag	cgt	gag	atc	1100
Arg	Lys	Arg	Lys	Ser	Cys	Tyr	Gly	Tyr	Asn	Ala	Trp	Gln	Arg	Glu	Ile	
	275					280					285					
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Ile	Tyr	Lys	Arg	Arg	Arg	Ser	Pro	Asp	Arg	Ser	Ser	Val	Val	Thr	Ser	
290					295					300					305	



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 Gly Arg Trp Arg Asp Val Lys Leu Arg Ala Phe Glu Asp Ala Asp His  
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cgg act tac gtg gac ttg aag gac aaa tgg aag acg cta gtt cac aca 1916  
 Arg Thr Tyr Val Asp Leu Lys Asp Lys Trp Lys Thr Leu Val His Thr  
 550 555 560

gca agt ata tcc cca cag caa cga aga gga gag ccg gtg cca caa gaa 1964  
 Ala Ser Ile Ser Pro Gln Gln Arg Arg Gly Glu Pro Val Pro Gln Glu  
 565 570 575

ctg cta gac aga gtc ttg agg gca tac ggg tat tgg tcg cag cac caa 2012  
 Leu Leu Asp Arg Val Leu Arg Ala Tyr Gly Tyr Trp Ser Gln His Gln  
 580 585 590

gga aaa cat cag gcg aga gga gcg tcc aaa gat cca gac atg aac aga 2060  
 Gly Lys His Gln Ala Arg Gly Ala Ser Lys Asp Pro Asp Met Asn Arg  
 595 600 605

ggg gga gct ttt gaa tca ggt gtt tca gtgtaaaaaa ggaggtacgc 2107  
 Gly Gly Ala Phe Glu Ser Gly Val Ser  
 610 615

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agtttaattg tctttatttc tcgttttttt ttttttttct cctacataca cttttttttt 2227

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 35 40 45

Leu Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser  
 50 55 60

Ala Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn  
 65 70 75 80

Cys Lys Thr Ile Lys Ser Glu Ser Ser Asp Gln Gly Asn Ser Val Ser  
 85 90 95  
 Lys Pro Thr Tyr Asp Ile Ser Thr Glu Lys Cys Val Val Asn Ser Cys  
 100 105 110  
 Phe Ser Phe Pro Asp Ser Asp Gly Val Leu Glu Arg Thr Pro Met Ser  
 115 120 125  
 Asp Tyr Lys Lys Ile His Gly Leu Met Asp Val Gly Cys Glu Asn Lys  
 130 135 140  
 Asn Val Asn Asn Gly Phe Glu Gln Gly Glu Ala Thr Asp Arg Val Gly  
 145 150 155 160  
 Asp Gly Gly Leu Val Thr Asp Thr Cys Asn Leu Glu Asp Ala Thr Ala  
 165 170 175  
 Leu Gly Leu Gln Phe Pro Lys Ser Val Cys Val Gly Gly Asp Leu Lys  
 180 185 190  
 Ser Pro Ser Thr Leu Asp Met Thr Pro Asn Gly Ser Tyr Ala Arg His  
 195 200 205  
 Gly Asn His Thr Asn Leu Gly Arg Lys Asp Asp Asp Glu Lys Phe Tyr  
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 Ser Tyr His Lys Leu Ser Asn Lys Phe Lys Ser Tyr Arg Cys Pro Thr  
 225 230 235 240  
 Ile Arg Arg Ile Arg Lys Ser Met Ser Ser Lys Tyr Trp Lys Gln Val  
 245 250 255  
 Pro Lys Asp Phe Gly Tyr Ser Arg Ala Asp Val Gly Val Lys Thr Leu  
 260 265 270  
 Tyr Arg Lys Arg Lys Ser Cys Tyr Gly Tyr Asn Ala Trp Gln Arg Glu  
 275 280 285  
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 370 375 380

166160:616160





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 Cys Asn Ile Gly Ser Pro Asp Glu Ser Thr Gly Glu Glu Arg Leu Ser  
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aag aag cct cga ttg gtg aga ggt gca gct ggt tat aca cct gat att 899  
 Lys Lys Pro Arg Leu Val Arg Gly Ala Ala Gly Tyr Thr Pro Asp Ile  
 225 230 235 240

gta gtg ggt cac cca ata cta gaa tca ggc ttg aac act tct tac cat 947  
 Val Val Gly His Pro Ile Leu Glu Ser Gly Leu Asn Thr Ser Tyr His  
 245 250 255

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 260 265 270

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 275 280 285

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 35 40 45  
 Val Met Gly Val Gln Gly Leu Thr Ile Tyr His Val Lys Ser His Leu  
 50 55 60  
 Gln Lys Tyr Arg Leu Ala Lys Tyr Leu Pro Asp Ser Ser Ser Glu Gly  
 65 70 75 80  
 Lys Lys Thr Asp Lys Lys Glu Ser Gly Asp Met Leu Ser Gly Leu Asp  
 85 90 95  
 Gly Ser Ser Gly Met Gln Ile Thr Glu Ala Leu Lys Leu Gln Met Glu  
 100 105 110





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Ser Ala Ile Arg Ser Ser Leu Pro Leu Asp Gly Ser Leu Gly Asp Tyr	
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Ser Asp Gly Thr Asn Leu Pro Ile Asp Ala Cys Leu Val Leu Thr Thr	
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gac ccc aag cct cgc ctt cgt tgg acc tct gag ctc cat gaa aga ttc	261
Asp Pro Lys Pro Arg Leu Arg Trp Thr Ser Glu Leu His Glu Arg Phe	
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Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr Pro Lys	
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Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr His Leu	
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Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys Lys Glu	
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Ser Ile Asp Asn Ser Lys Asp Val Ser Cys Val Ala Glu Ser Gln Asp	
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Thr Gly Ser Ser Ser Thr Ser Ser Leu Arg Leu Ala Ala Gln Glu Gln	
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Asn Glu Ser Tyr Gln Val Thr Glu Ala Leu Arg Ala Gln Met Glu Val	
135 140 145	
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Gln Arg Arg Leu His Glu Gln Leu Glu Val Gln Arg Arg Leu Gln Leu	
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Arg Ile Glu Ala Gln Gly Lys Tyr Leu Gln Ser Ile Leu Glu Lys Ala	
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Cys Lys Ala Ile Glu Glu Gln Ala Val Ala Phe Ala Gly Leu Glu Ala	
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Ala Arg Glu Glu Leu Ser Glu Leu Ala Ile Lys Ala Ser Ile Thr Asn	
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Gly Cys Gln Gly Thr Thr Ser Thr Phe Asp Thr Thr Lys Met Met Ile	
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 Pro Ser Leu Ser Glu Leu Ala Val Ala Ile Glu His Lys Asn Asn Cys  
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tca gca gag agc tct ctg act tcc agc act gta gga agt ccg gta tca 885  
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                   245                                  250                                  255

gct gcg ttg atg aag aag aga caa cga gga gtg ttt gga aat gga gat 933  
 Ala Ala Leu Met Lys Lys Arg Gln Arg Gly Val Phe Gly Asn Gly Asp  
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agt gtg gtt gtt ggt cat gat gct gga tgg gtt atg cct agt agt agc 981  
 Ser Val Val Val Gly His Asp Ala Gly Trp Val Met Pro Ser Ser Ser  
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tatatatttg ttgaatctaa aaaaaa 1123

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 Met Tyr Ser Ala Ile Arg Ser Ser Leu Pro Leu Asp Gly Ser Leu Gly  
   1                                  5                                  10                                  15

Asp Tyr Ser Asp Gly Thr Asn Leu Pro Ile Asp Ala Cys Leu Val Leu  
                   20                                  25                                  30

Thr Thr Asp Pro Lys Pro Arg Leu Arg Trp Thr Ser Glu Leu His Glu  
                   35                                  40                                  45

Arg Phe Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr  
                   50                                  55                                  60

Pro Lys Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr  
                   65                                  70                                  75                                  80

His Leu Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys  
                   85                                  90                                  95

Lys Glu Ser Ile Asp Asn Ser Lys Asp Val Ser Cys Val Ala Glu Ser  
                   100                                  105                                  110

Gln Asp Thr Gly Ser Ser Ser Thr Ser Ser Leu Arg Leu Ala Ala Gln  
                   115                                  120                                  125

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[illegible]